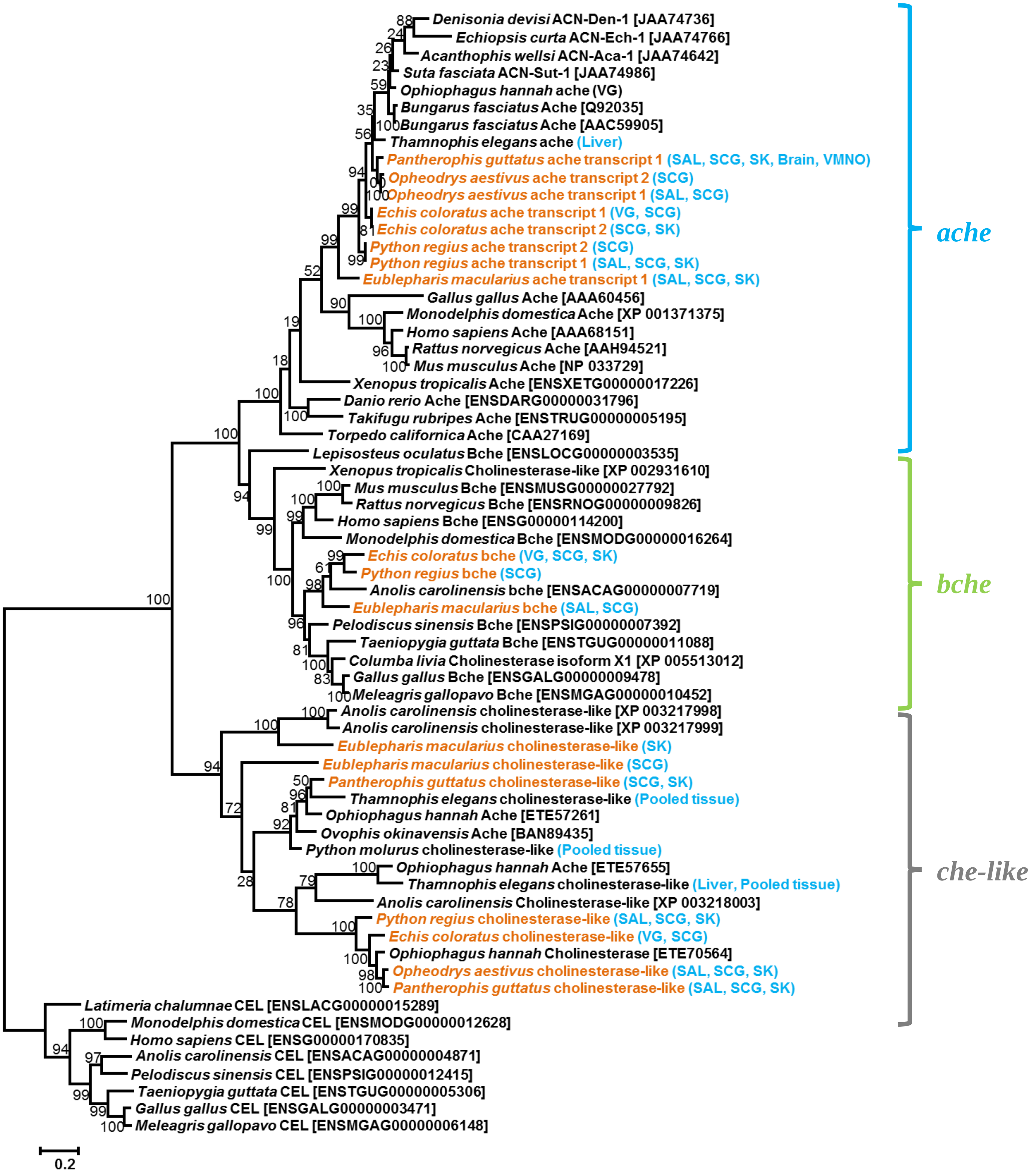
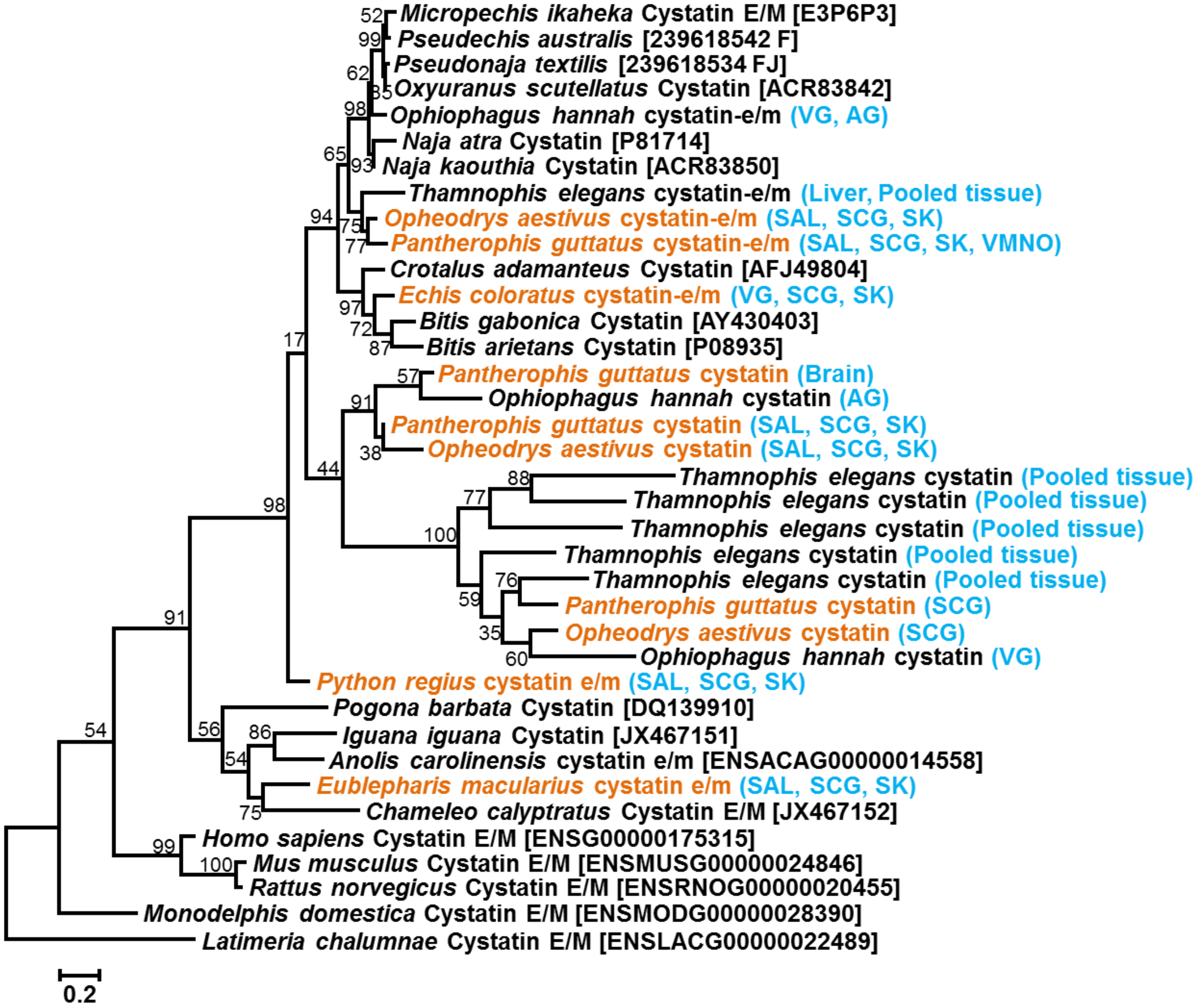

Denisonia devisi ACN-Den-1 [JAA74736]
Echiopsis curta ACN-Ech-1 [JAA74766]
Acanthophis wellsi ACN-Aca-1 [JAA74642]
Suta fasciata ACN-Sut-1 [JAA74986]
Ophiophagus hannah ache (VG)
Bungarus fasciatus Ache [Q92035]
Bungarus fasciatus Ache [AAC59905]
Thamnophis elegans ache (Liver)
Pantherophis guttatus ache transcript 1 (SAL, SCG, SK, Brain, VMNO)
Opheodrys aestivus ache transcript 2 (SCG)
Opheodrys aestivus ache transcript 1 (SAL, SCG)
Echis coloratus ache transcript 1 (VG, SCG)
Echis coloratus ache transcript 2 (SCG, SK)
Python regius ache transcript 2 (SCG)
Python regius ache transcript 1 (SAL, SCG, SK)
Eublepharis macularius ache transcript 1 (SAL, SCG, SK)
Gallus gallus Ache [AAA60456]
Monodelphis domestica Ache [XP 001371375]
Homo sapiens Ache [AAA68151]
Rattus norvegicus Ache [AAH94521]
Mus musculus Ache [NP 033729]
Xenopus tropicalis Ache [ENSXETG00000017226]
Danio rerio Ache [ENSDARG00000031796]
Takifugu rubripes Ache [ENSTRUG00000005195]
Torpedo californica Ache [CAA27169]
Lepisosteus oculatus Bche [ENSLOCG00000003535]
Xenopus tropicalis Cholinesterase-like [XP 002931610]
Mus musculus Bche [ENSMUSG00000027792]
Rattus norvegicus Bche [ENSRNOG00000009826]
Homo sapiens Bche [ENSG00000114200]
Monodelphis domestica Bche [ENSMODG00000016264]
Echis coloratus bche (VG, SCG, SK)
Python regius bche (SCG)
Anolis carolinensis bche [ENSACAG00000007719]
Eublepharis macularius bche (SAL, SCG)
Pelodiscus sinensis Bche [ENSPSIG00000007392]
Taeniopygia guttata Bche [ENSTGUG00000011088]
Columba livia Cholinesterase isoform X1 [XP 005513012]
Gallus gallus Bche [ENSGALG00000009478]
Meleagris gallopavo Bche [ENSMGAG00000010452]
Anolis carolinensis cholinesterase-like [XP 003217998]
Anolis carolinensis cholinesterase-like [XP 003217999]
Eublepharis macularius cholinesterase-like (SK)
Eublepharis macularius cholinesterase-like (SCG)
Pantherophis guttatus cholinesterase-like (SCG, SK)
Thamnophis elegans cholinesterase-like (Pooled tissue)
Ophiophagus hannah Ache [ETE57261]
Ovophis okinavensis Ache [BAN89435]
Python molurus cholinesterase-like (Pooled tissue)
Ophiophagus hannah Ache [ETE57655]
Thamnophis elegans cholinesterase-like (Liver, Pooled tissue)
Anolis carolinensis Cholinesterase-like [XP 003218003]
Python regius cholinesterase-like (SAL, SCG, SK)
Echis coloratus cholinesterase-like (VG, SCG)
Ophiophagus hannah Cholinesterase [ETE70564]
Opheodrys aestivus cholinesterase-like (SAL, SCG, SK)
Pantherophis guttatus cholinesterase-like (SAL, SCG, SK)
Latimeria chalumnae CEL [ENSLACG00000015289]
Monodelphis domestica CEL [ENSMODG00000012628]
Homo sapiens CEL [ENSG00000170835]
Anolis carolinensis CEL [ENSACAG00000004871]
Pelodiscus sinensis CEL [ENSPSIG00000012415]
Taeniopygia guttata CEL [ENSTGUG00000005306]
Gallus gallus CEL [ENSGALG00000003471]
Meleagris gallopavo CEL [ENSMGAG00000006148]
ache
bche
che-like
0.2

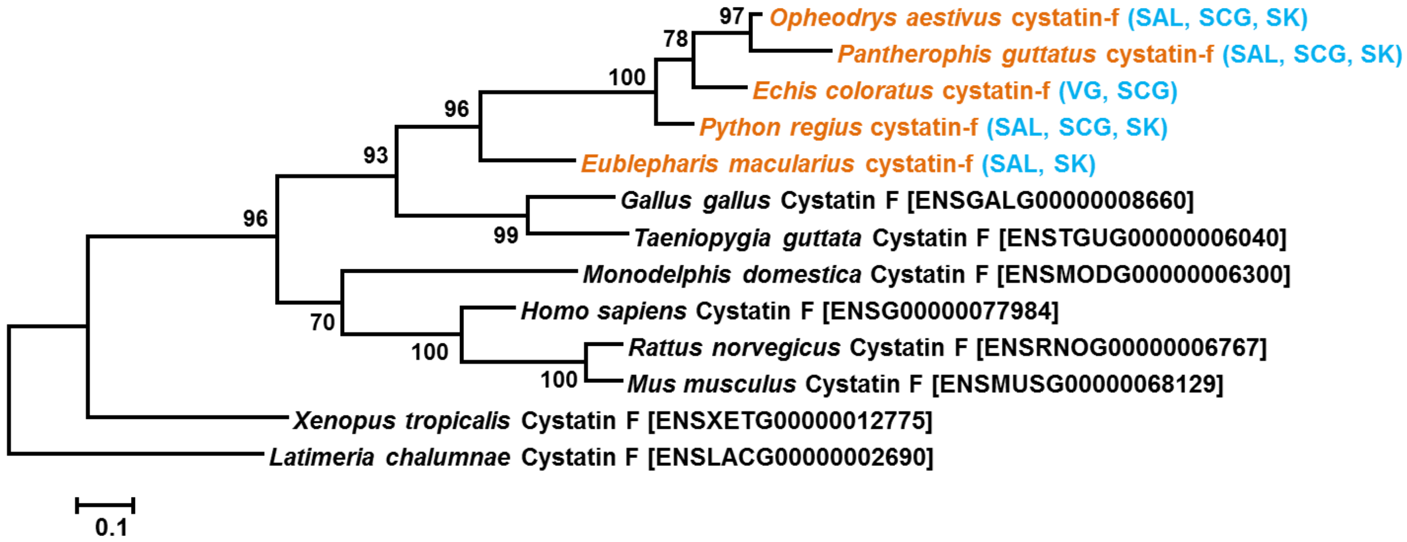
Supplementary figure S1

Maximum likelihood tree of *acetylcholinesterase* (*ache*), *butyrylcholinesterase* (*bche*) and *cholinesterase-like* sequences. Genbank accession numbers or Ensembl gene IDs are given in square brackets. Sequences from this study are in orange text and the location of transcripts is provided in bracketed blue text (VG, venom gland; SAL, salivary gland; SK, skin; SCG, scent gland; VMNO, vomeronasal organ). Numbers above branches correspond to Bootstrap values for 500 replicates.


52
Micropechis ikaheka Cystatin E/M [E3P6P3]
99
Pseudechis australis [239618542 F]
62
Pseudonaja textilis [239618534 FJ]
35
Oxyuranus scutellatus Cystatin [ACR83842]
98
Ophiophagus hannah cystatin-e/m (VG, AG)
65
Naja atra Cystatin [P81714]
93
Naja kaouthia Cystatin [ACR83850]
Thamnophis elegans cystatin-e/m (Liver, Pooled tissue)
94
75
Opheodrys aestivus cystatin-e/m (SAL, SCG, SK)
77
Pantherophis guttatus cystatin-e/m (SAL, SCG, SK, VMNO)
Crotalus adamanteus Cystatin [AFJ49804]
Echis coloratus cystatin-e/m (VG, SCG, SK)
97
72
Bitis gabonica Cystatin [AY430403]
87
Bitis arietans Cystatin [P08935]
17
57
Pantherophis guttatus cystatin (Brain)
91
Ophiophagus hannah cystatin (AG)
Pantherophis guttatus cystatin (SAL, SCG, SK)
38
Opheodrys aestivus cystatin (SAL, SCG, SK)
44
88
Thamnophis elegans cystatin (Pooled tissue)
77
Thamnophis elegans cystatin (Pooled tissue)
98
Thamnophis elegans cystatin (Pooled tissue)
100
Thamnophis elegans cystatin (Pooled tissue)
76
Thamnophis elegans cystatin (Pooled tissue)
59
Pantherophis guttatus cystatin (SCG)
91
35
Opheodrys aestivus cystatin (SCG)
60
Ophiophagus hannah cystatin (VG)
Python regius cystatin e/m (SAL, SCG, SK)
Pogona barbata Cystatin [DQ139910]
56
86
Iguana iguana Cystatin [JX467151]
54
54
Anolis carolinensis cystatin e/m [ENSACAG00000014558]
Eublepharis macularius cystatin e/m (SAL, SCG, SK)
75
Chameleo calyptratus Cystatin E/M [JX467152]
99
Homo sapiens Cystatin E/M [ENSG00000175315]
100
Mus musculus Cystatin E/M [ENSMUSG00000024846]
Rattus norvegicus Cystatin E/M [ENSRNOG00000020455]
Monodelphis domestica Cystatin E/M [ENSMODG00000028390]
Latimeria chalumnae Cystatin E/M [ENSLACG00000022489]
0.2

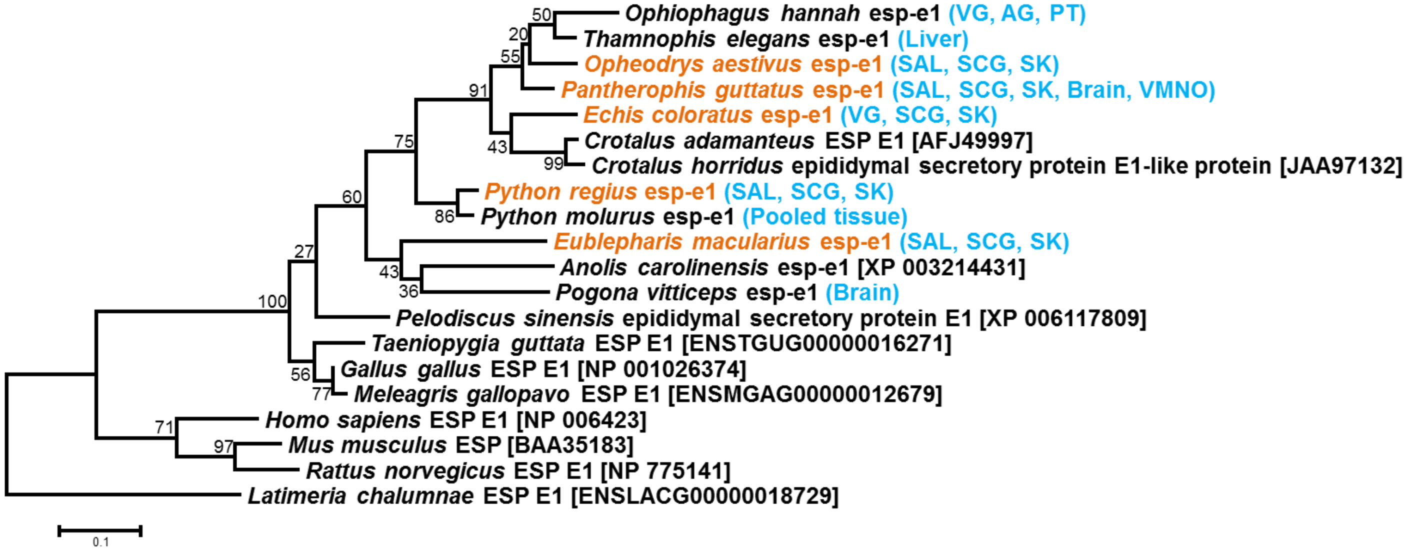
Supplementary figure S2

Maximum likelihood tree of *cystatin-e/m* sequences. Genbank accession numbers or Ensembl gene IDs are given in square brackets. Sequences from this study are in orange text and the location of transcripts is provided in bracketed blue text (VG, venom gland; SAL, salivary gland; SK, skin; SCG, scent gland; AG, accessory gland; VMNO, vomeronasal organ). Numbers above branches correspond to Bootstrap values for 500 replicates.


97
78
100
96
93
96
99
70
100
100
Opheodrys aestivus cystatin-f (SAL, SCG, SK)
Pantherophis guttatus cystatin-f (SAL, SCG, SK)
Echis coloratus cystatin-f (VG, SCG)
Python regius cystatin-f (SAL, SCG, SK)
Eublepharis macularius cystatin-f (SAL, SK)
Gallus gallus Cystatin F [ENSGALG00000008660]
Taeniopygia guttata Cystatin F [ENSTGUG00000006040]
Monodelphis domestica Cystatin F [ENSMODG00000006300]
Homo sapiens Cystatin F [ENSG00000077984]
Rattus norvegicus Cystatin F [ENSRNOG00000006767]
Mus musculus Cystatin F [ENSMUSG00000068129]
Xenopus tropicalis Cystatin F [ENSXETG00000012775]
Latimeria chalumnae Cystatin F [ENSLACG00000002690]
0.1

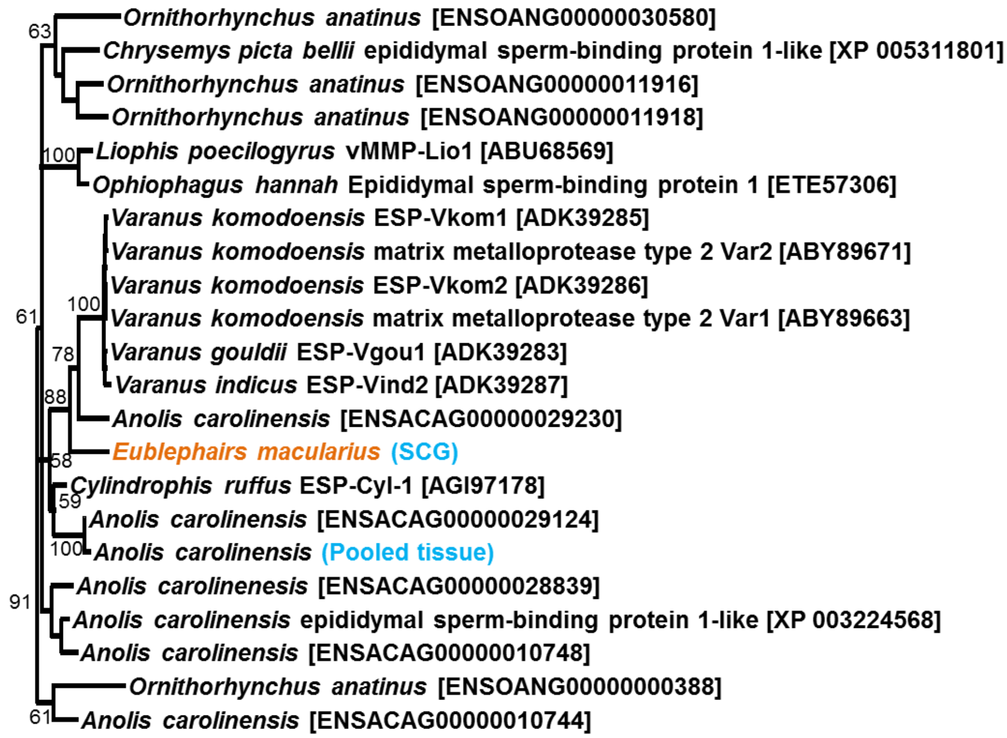
Supplementary figure S3

Maximum likelihood tree of *cystatin-f* sequences. Genbank accession numbers or Ensembl gene IDs are given in square brackets. Sequences from this study are in orange text and the location of transcripts is provided in bracketed blue text (VG, venom gland; SAL, salivary gland; SK, skin; SCG, scent gland). Numbers above branches correspond to Bootstrap values for 500 replicates.


Ophiophagus hannah esp-e1 (VG, AG, PT)
Thamnophis elegans esp-e1 (Liver)
Opheodrys aestivus esp-e1 (SAL, SCG, SK)
Pantherophis guttatus esp-e1 (SAL, SCG, SK, Brain, VMNO)
Echis coloratus esp-e1 (VG, SCG, SK)
Crotalus adamanteus ESP E1 [AFJ49997]
Crotalus horridus epididymal secretory protein E1-like protein [JAA97132]
Python regius esp-e1 (SAL, SCG, SK)
Python molurus esp-e1 (Pooled tissue)
Eublepharis macularius esp-e1 (SAL, SCG, SK)
Anolis carolinensis esp-e1 [XP 003214431]
Pogona vitticeps esp-e1 (Brain)
Pelodiscus sinensis epididymal secretory protein E1 [XP 006117809]
Taeniopygia guttata ESP E1 [ENSTGUG00000016271]
Gallus gallus ESP E1 [NP 001026374]
Meleagris gallopavo ESP E1 [ENSMGAG00000012679]
Homo sapiens ESP E1 [NP 006423]
Mus musculus ESP [BAA35183]
Rattus norvegicus ESP E1 [NP 775141]
Latimeria chalumnae ESP E1 [ENSLACG00000018729]
50
20
55
91
43
99
75
86
60
43
36
27
100
56
77
71
97
0.1

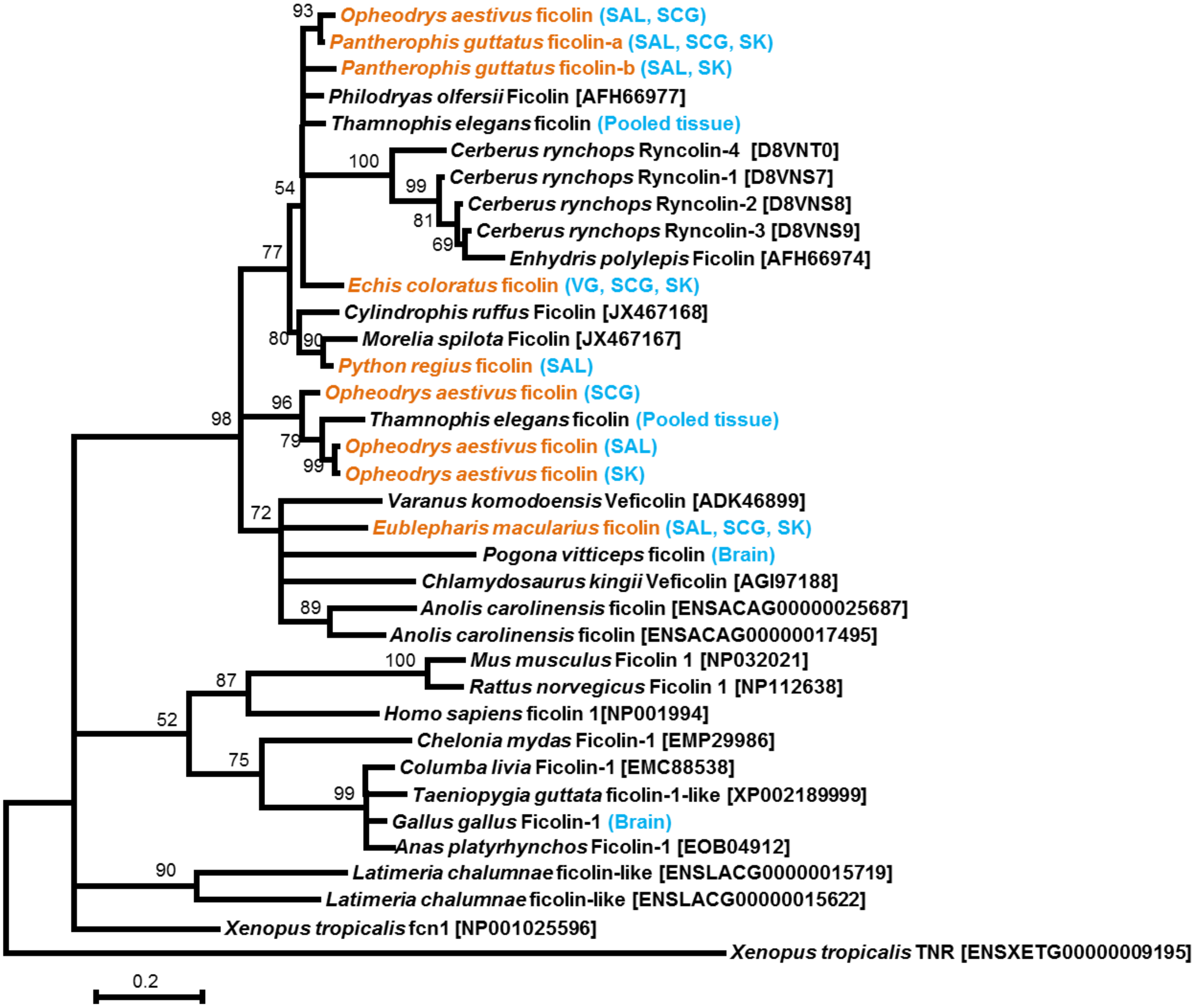
Supplementary figure S4a

Maximum likelihood tree of *epididymal secretory protein e1* (*esp-e1*) sequences. Genbank accession numbers or Ensembl gene IDs are given in square brackets. Sequences from this study are in orange text and the location of transcripts is provided in bracketed blue text (VG, venom gland; SAL, salivary gland; SK, skin; SCG, scent gland; AG, accessory gland; PT, pooled tissue; VMNO, vomeronasal organ). Numbers above branches correspond to Bootstrap values for 500 replicates.


Ornithorhynchus anatinus [ENSOANG00000030580]
Chrysemys picta bellii epididymal sperm-binding protein 1-like [XP 005311801]
Ornithorhynchus anatinus [ENSOANG00000011916]
Ornithorhynchus anatinus [ENSOANG00000011918]
Liophis poecilogyrus vMMP-Lio1 [ABU68569]
Ophiophagus hannah Epididymal sperm-binding protein 1 [ETE57306]
Varanus komodoensis ESP-Vkom1 [ADK39285]
Varanus komodoensis matrix metalloprotease type 2 Var2 [ABY89671]
Varanus komodoensis ESP-Vkom2 [ADK39286]
Varanus komodoensis matrix metalloprotease type 2 Var1 [ABY89663]
Varanus gouldii ESP-Vgou1 [ADK39283]
Varanus indicus ESP-Vind2 [ADK39287]
Anolis carolinensis [ENSACAG00000029230]
Eublephairs macularius (SCG)
Cylindrophis ruffus ESP-Cyl-1 [AGI97178]
Anolis carolinensis [ENSACAG00000029124]
Anolis carolinensis (Pooled tissue)
Anolis carolinenesis [ENSACAG00000028839]
Anolis carolinensis epididymal sperm-binding protein 1-like [XP 003224568]
Anolis carolinensis [ENSACAG00000010748]
Ornithorhynchus anatinus [ENSOANG00000000388]
Anolis carolinensis [ENSACAG00000010744]
63
100
100
61
78
88
58
59
100
91
61

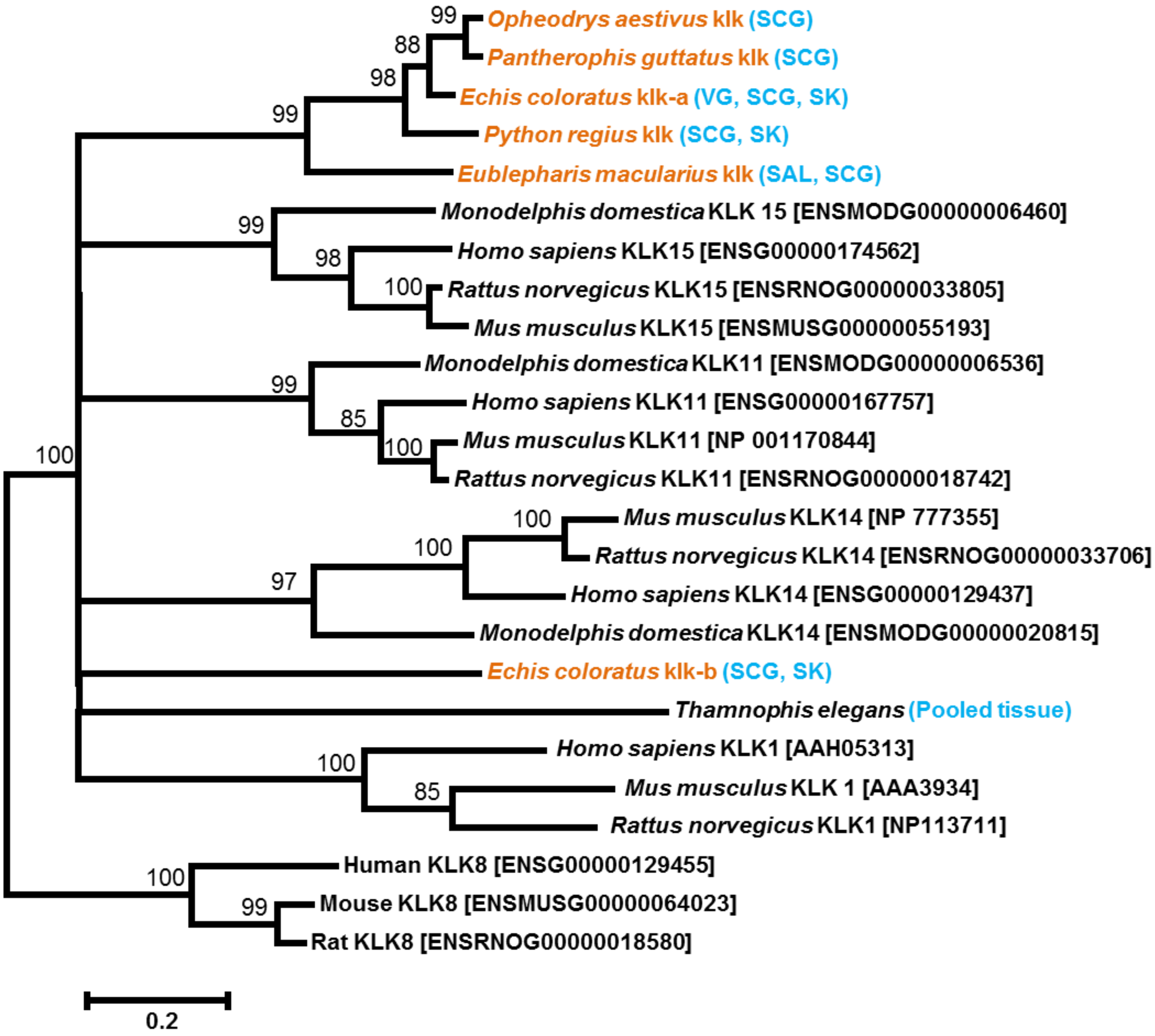
Supplementary figure S4b

Maximum likelihood tree of *epididymal secretory protein* sequences. Genbank accession numbers or Ensembl gene IDs are given in square brackets. Sequences from this study are in orange text and the location of transcripts is provided in bracketed blue text (SCG, scent gland). Numbers above branches correspond to Bootstrap values for 500 replicates.


93
Opheodrys aestivus ficolin (SAL, SCG)
Pantherophis guttatus ficolin-a (SAL, SCG, SK)
Pantherophis guttatus ficolin-b (SAL, SK)
Philodryas olfersii Ficolin [AFH66977]
Thamnophis elegans ficolin (Pooled tissue)
100
Cerberus rynchops Ryncolin-4 [D8VNT0]
99
Cerberus rynchops Ryncolin-1 [D8VNS7]
54
81
Cerberus rynchops Ryncolin-2 [D8VNS8]
69
Cerberus rynchops Ryncolin-3 [D8VNS9]
Enhydris polylepis Ficolin [AFH66974]
77
Echis coloratus ficolin (VG, SCG, SK)
Cylindrophis ruffus Ficolin [JX467168]
80
90
Morelia spilota Ficolin [JX467167]
Python regius ficolin (SAL)
Opheodrys aestivus ficolin (SCG)
96
98
Thamnophis elegans ficolin (Pooled tissue)
79
Opheodrys aestivus ficolin (SAL)
99
Opheodrys aestivus ficolin (SK)
Varanus komodoensis Veficolin [ADK46899]
72
Eublepharis macularius ficolin (SAL, SCG, SK)
Pogona vitticeps ficolin (Brain)
Chlamydosaurus kingii Veficolin [AGI97188]
89
Anolis carolinensis ficolin [ENSACAG00000025687]
Anolis carolinensis ficolin [ENSACAG00000017495]
100
Mus musculus Ficolin 1 [NP032021]
87
Rattus norvegicus Ficolin 1 [NP112638]
52
Homo sapiens ficolin 1[NP001994]
Chelonia mydas Ficolin-1 [EMP29986]
75
Columba livia Ficolin-1 [EMC88538]
99
Taeniopygia guttata ficolin-1-like [XP002189999]
Gallus gallus Ficolin-1 (Brain)
Anas platyrhynchos Ficolin-1 [EOB04912]
90
Latimeria chalumnae ficolin-like [ENSLACG00000015719]
Latimeria chalumnae ficolin-like [ENSLACG00000015622]
Xenopus tropicalis fcn1 [NP001025596]
Xenopus tropicalis TNR [ENSXETG00000009195]
0.2

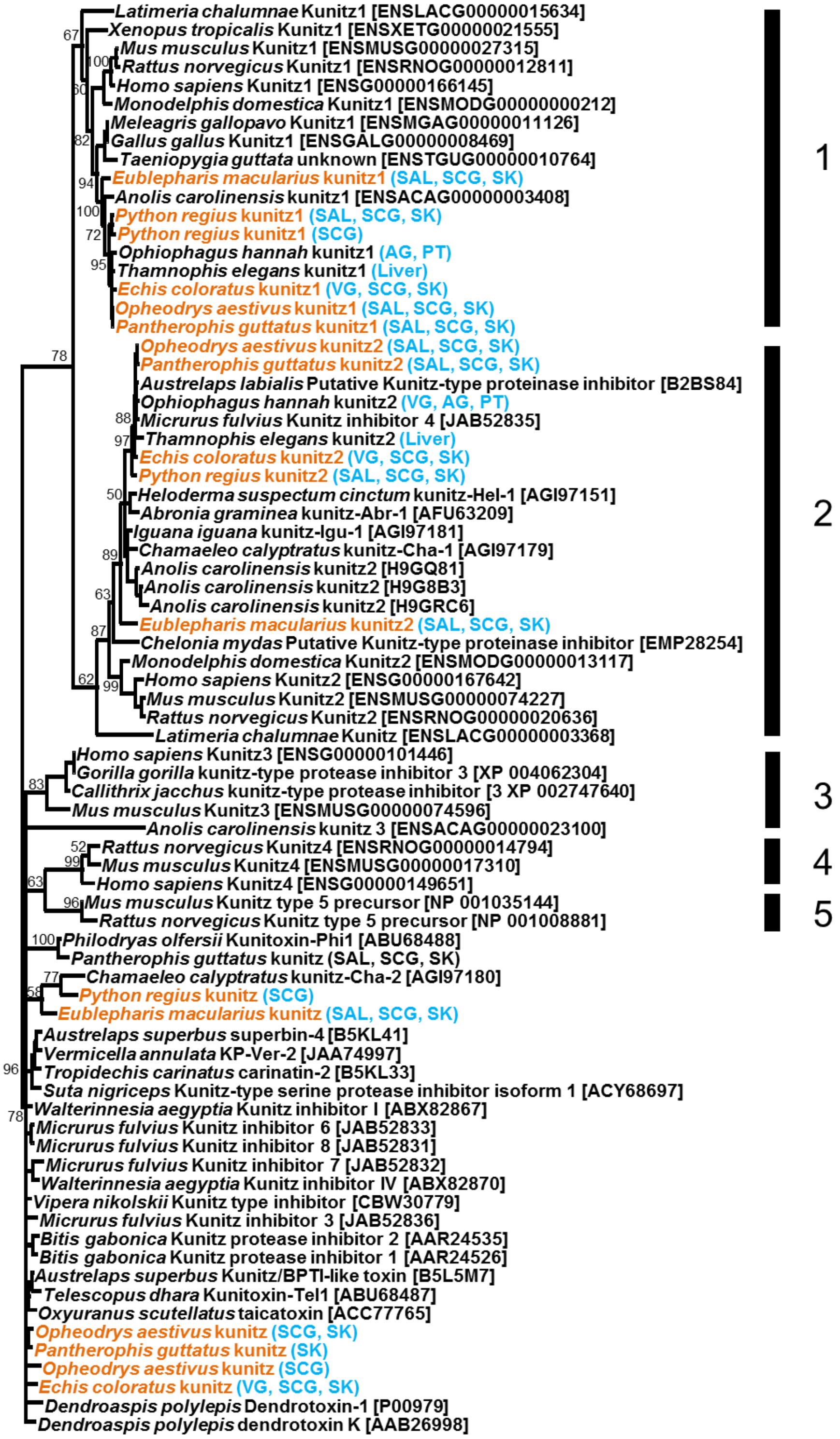
Supplementary figure S5

Maximum likelihood tree of *ficolin* sequences. Genbank accession numbers or Ensembl gene IDs are given in square brackets. Sequences from this study are in orange text and the location of transcripts is provided in bracketed blue text (VG, venom gland; SAL, salivary gland; SK, skin; SCG, scent gland). Numbers above branches correspond to Bootstrap values for 500 replicates.


99
88
98
99
Opheodrys aestivus klk (SCG)
Pantherophis guttatus klk (SCG)
Echis coloratus klk-a (VG, SCG, SK)
Python regius klk (SCG, SK)
Eublepharis macularius klk (SAL, SCG)
99
98
100
Monodelphis domestica KLK 15 [ENSMODG00000006460]
Homo sapiens KLK15 [ENSG00000174562]
Rattus norvegicus KLK15 [ENSRNOG00000033805]
Mus musculus KLK15 [ENSMUSG00000055193]
99
85
100
Monodelphis domestica KLK11 [ENSMODG00000006536]
Homo sapiens KLK11 [ENSG00000167757]
Mus musculus KLK11 [NP 001170844]
Rattus norvegicus KLK11 [ENSRNOG00000018742]
100
100
100
97
Mus musculus KLK14 [NP 777355]
Rattus norvegicus KLK14 [ENSRNOG00000033706]
Homo sapiens KLK14 [ENSG00000129437]
Monodelphis domestica KLK14 [ENSMODG00000020815]
Echis coloratus klk-b (SCG, SK)
Thamnophis elegans (Pooled tissue)
100
85
Homo sapiens KLK1 [AAH05313]
Mus musculus KLK 1 [AAA3934]
Rattus norvegicus KLK1 [NP113711]
100
99
Human KLK8 [ENSG00000129455]
Mouse KLK8 [ENSMUSG00000064023]
Rat KLK8 [ENSRNOG00000018580]
0.2

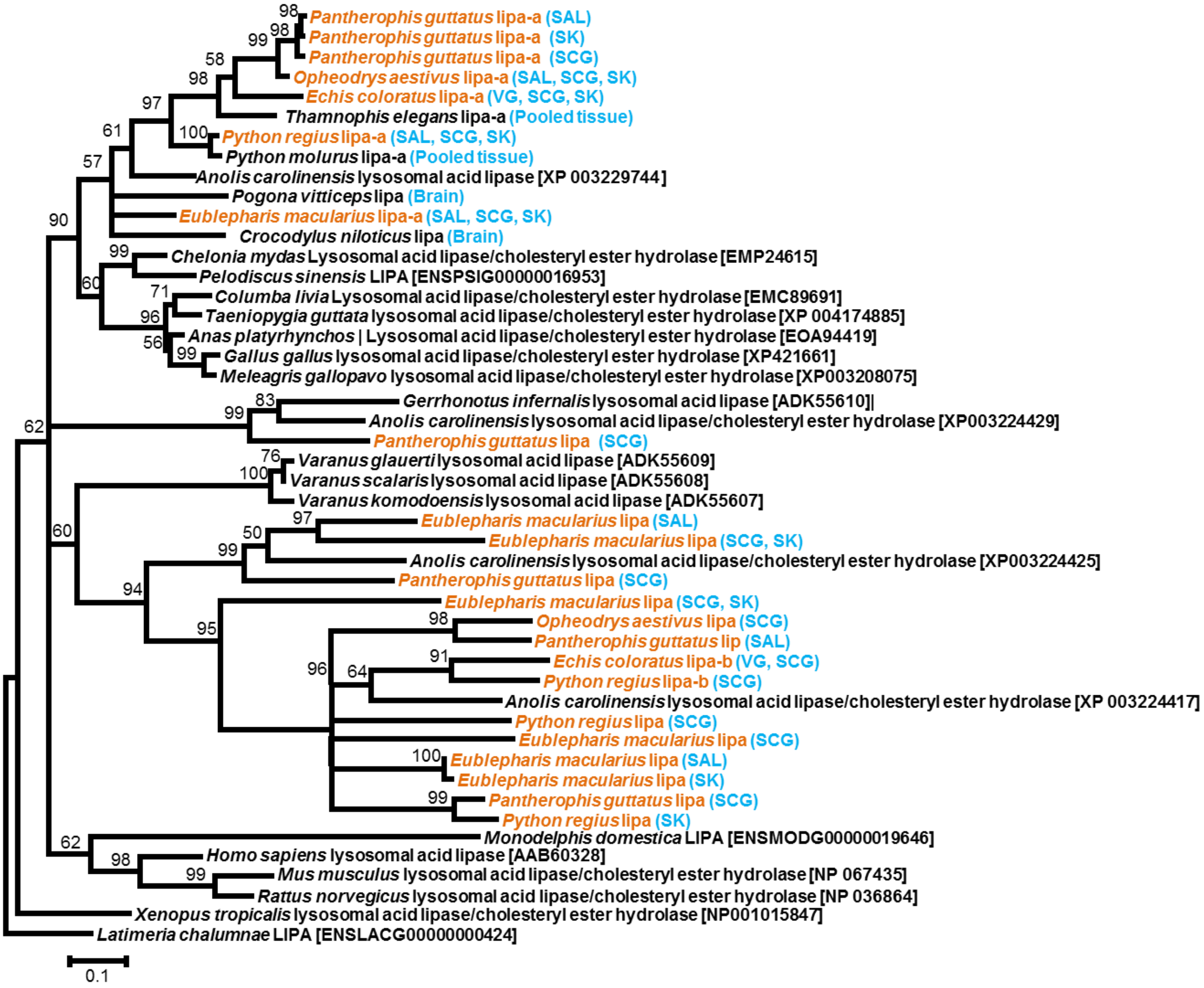
Supplementary figure S6

Maximum likelihood tree of *kallikrein* (*klk*) sequences. Genbank accession numbers or Ensembl gene IDs are given in square brackets. Sequences from this study are in orange text and the location of transcripts is provided in bracketed blue text (VG, venom gland; SAL, salivary gland; SK, skin; SCG, scent gland). Numbers above branches correspond to Bootstrap values for 500 replicates.


Latimeria chalumnae Kunitz1 [ENSLACG00000015634]
Xenopus tropicalis Kunitz1 [ENSXETG00000021555]
Mus musculus Kunitz1 [ENSMUSG00000027315]
Rattus norvegicus Kunitz1 [ENSRNOG00000012811]
Homo sapiens Kunitz1 [ENSG00000166145]
Monodelphis domestica Kunitz1 [ENSMODG00000000212]
Meleagris gallopavo Kunitz1 [ENSMGAG00000011126]
Gallus gallus Kunitz1 [ENSGALG00000008469]
Taeniopygia guttata unknown [ENSTGUG00000010764]
Eublepharis macularius kunitz1 (SAL, SCG, SK)
Anolis carolinensis kunitz1 [ENSACAG00000003408]
Python regius kunitz1 (SAL, SCG, SK)
Python regius kunitz1 (SCG)
Ophiophagus hannah kunitz1 (AG, PT)
Thamnophis elegans kunitz1 (Liver)
Echis coloratus kunitz1 (VG, SCG, SK)
Opheodrys aestivus kunitz1 (SAL, SCG, SK)
Pantherophis guttatus kunitz1 (SAL, SCG, SK)
Opheodrys aestivus kunitz2 (SAL, SCG, SK)
Pantherophis guttatus kunitz2 (SAL, SCG, SK)
Austrelaps labialis Putative Kunitz-type proteinase inhibitor [B2BS84]
Ophiophagus hannah kunitz2 (VG, AG, PT)
Micrurus fulvius Kunitz inhibitor 4 [JAB52835]
Thamnophis elegans kunitz2 (Liver)
Echis coloratus kunitz2 (VG, SCG, SK)
Python regius kunitz2 (SAL, SCG, SK)
Heloderma suspectum cinctum kunitz-Hel-1 [AGI97151]
Abronia graminea kunitz-Abr-1 [AFU63209]
Iguana iguana kunitz-Igu-1 [AGI97181]
Chamaeleo calyptratus kunitz-Cha-1 [AGI97179]
Anolis carolinensis kunitz2 [H9GQ81]
Anolis carolinensis kunitz2 [H9G8B3]
Anolis carolinensis kunitz2 [H9GRC6]
Eublepharis macularius kunitz2 (SAL, SCG, SK)
Chelonia mydas Putative Kunitz-type proteinase inhibitor [EMP28254]
Monodelphis domestica Kunitz2 [ENSMODG00000013117]
Homo sapiens Kunitz2 [ENSG00000167642]
Mus musculus Kunitz2 [ENSMUSG00000074227]
Rattus norvegicus Kunitz2 [ENSRNOG00000020636]
Latimeria chalumnae Kunitz [ENSLACG00000003368]
Homo sapiens Kunitz3 [ENSG00000101446]
Gorilla gorilla kunitz-type protease inhibitor 3 [XP 004062304]
Callithrix jacchus kunitz-type protease inhibitor [3 XP 002747640]
Mus musculus Kunitz3 [ENSMUSG00000074596]
Anolis carolinensis kunitz 3 [ENSACAG00000023100]
Rattus norvegicus Kunitz4 [ENSRNOG00000014794]
Mus musculus Kunitz4 [ENSMUSG00000017310]
Homo sapiens Kunitz4 [ENSG00000149651]
Mus musculus Kunitz type 5 precursor [NP 001035144]
Rattus norvegicus Kunitz type 5 precursor [NP 001008881]
Philodryas olfersii Kunitoxin-Phi1 [ABU68488]
Pantherophis guttatus kunitz (SAL, SCG, SK)
Chamaeleo calyptratus kunitz-Cha-2 [AGI97180]
Python regius kunitz (SCG)
Eublepharis macularius kunitz (SAL, SCG, SK)
Austrelaps superbus superbin-4 [B5KL41]
Vermicella annulata KP-Ver-2 [JAA74997]
Tropidechis carinatus carinatin-2 [B5KL33]
Suta nigriceps Kunitz-type serine protease inhibitor isoform 1 [ACY68697]
Walterinnesia aegyptia Kunitz inhibitor I [ABX82867]
Micrurus fulvius Kunitz inhibitor 6 [JAB52833]
Micrurus fulvius Kunitz inhibitor 8 [JAB52831]
Micrurus fulvius Kunitz inhibitor 7 [JAB52832]
Walterinnesia aegyptia Kunitz inhibitor IV [ABX82870]
Vipera nikolskii Kunitz type inhibitor [CBW30779]
Micrurus fulvius Kunitz inhibitor 3 [JAB52836]
Bitis gabonica Kunitz protease inhibitor 2 [AAR24535]
Bitis gabonica Kunitz protease inhibitor 1 [AAR24526]
Austrelaps superbus Kunitz/BPTI-like toxin [B5L5M7]
Telescopus dhara Kunitoxin-Tel1 [ABU68487]
Oxyuranus scutellatus taicatoxin [ACC77765]
Opheodrys aestivus kunitz (SCG, SK)
Pantherophis guttatus kunitz (SK)
Opheodrys aestivus kunitz (SCG)
Echis coloratus kunitz (VG, SCG, SK)
Dendroaspis polylepis Dendrotoxin-1 [P00979]
Dendroaspis polylepis dendrotoxin K [AAB26998]
67
100
60
82
94
100
72
95
78
88
97
50
89
63
87
62
99
83
52
99
63
96
100
77
58
96
78
1
2
3
4
5

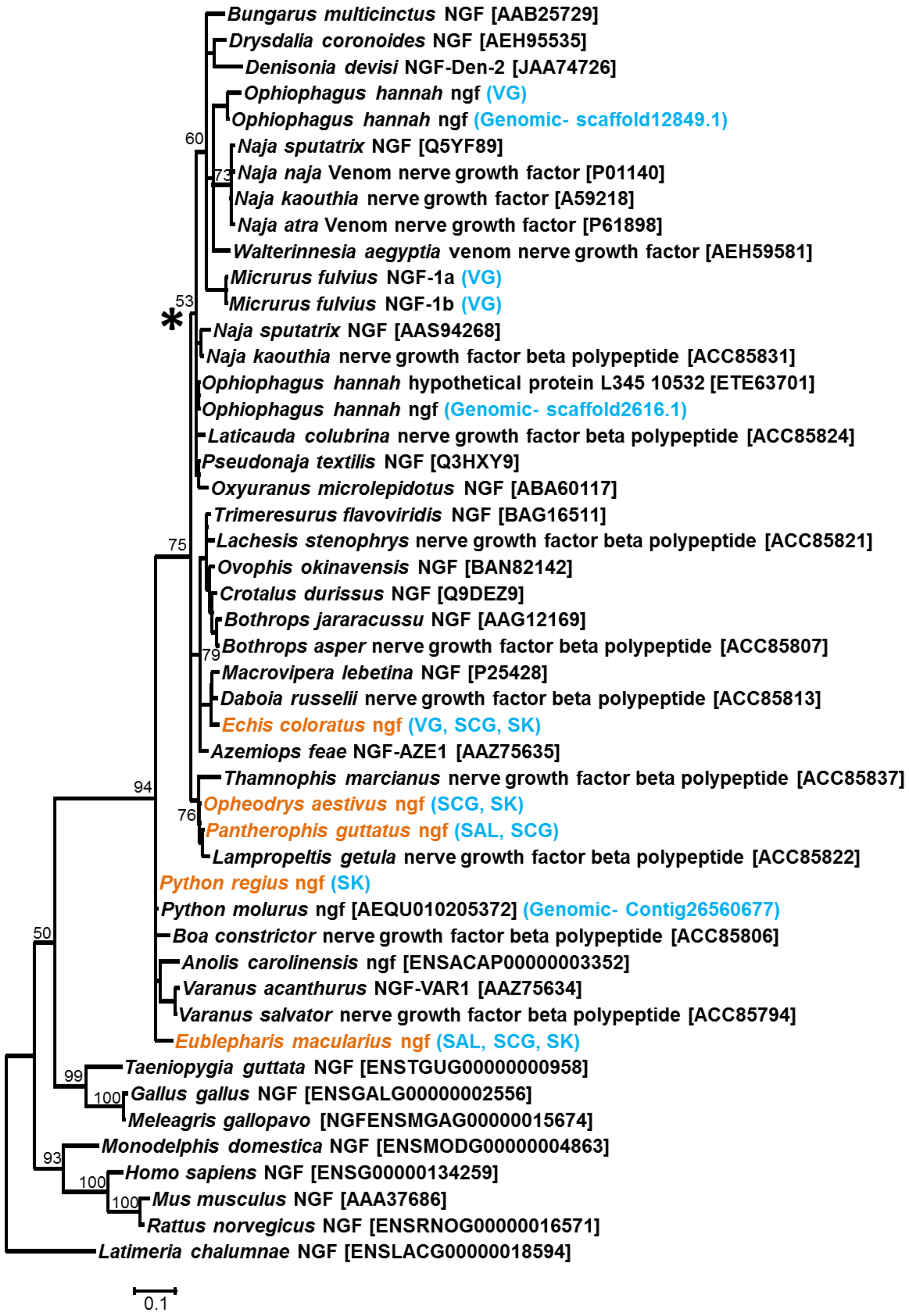
Supplementary figure S7

Maximum likelihood tree of *kunitz 1* and *2* sequences. Genbank accession numbers or Ensembl gene IDs are given in square brackets. The three kunitz2 sequences from the Green Anole (*Anolis carolinensis*) are derived from the genome of this species as used previously by Fry et al. [2]. Sequences from this study are in orange text and the location of transcripts is provided in bracketed blue text (VG, venom gland; SAL, salivary gland; SK, skin; SCG, scent gland; AG, accessory gland; PT, pooled tissue). Numbers above branches correspond to Bootstrap values for 500 replicates.


98 Pantherophis guttatus lipa-a (SAL)
99 98 Pantherophis guttatus lipa-a (SK)
Pantherophis guttatus lipa-a (SCG)
58
98 Opheodrys aestivus lipa-a (SAL, SCG, SK)
Echis coloratus lipa-a (VG, SCG, SK)
97
Thamnophis elegans lipa-a (Pooled tissue)
61
100 Python regius lipa-a (SAL, SCG, SK)
Python molurus lipa-a (Pooled tissue)
57
Anolis carolinensis lysosomal acid lipase [XP 003229744]
Pogona vitticeps lipa (Brain)
90
Eublepharis macularius lipa-a (SAL, SCG, SK)
Crocodylus niloticus lipa (Brain)
99 Chelonia mydas Lysosomal acid lipase/cholesteryl ester hydrolase [EMP24615]
60 Pelodiscus sinensis LIPA [ENSPSIG00000016953]
71 Columba livia Lysosomal acid lipase/cholesteryl ester hydrolase [EMC89691]
96 Taeniopygia guttata lysosomal acid lipase/cholesteryl ester hydrolase [XP 004174885]
56 Anas platyrhynchos | Lysosomal acid lipase/cholesteryl ester hydrolase [EOA94419]
99 Gallus gallus lysosomal acid lipase/cholesteryl ester hydrolase [XP421661]
Meleagris gallopavo lysosomal acid lipase/cholesteryl ester hydrolase [XP003208075]
83 Gerrhonotus infernalis lysosomal acid lipase [ADK55610]|
99 Anolis carolinensis lysosomal acid lipase/cholesteryl ester hydrolase [XP003224429]
62
Pantherophis guttatus lipa (SCG)
76 Varanus glauerti lysosomal acid lipase [ADK55609]
100 Varanus scalaris lysosomal acid lipase [ADK55608]
Varanus komodoensis lysosomal acid lipase [ADK55607]
97 Eublepharis macularius lipa (SAL)
60
50 Eublepharis macularius lipa (SCG, SK)
99 Anolis carolinensis lysosomal acid lipase/cholesteryl ester hydrolase [XP003224425]
Pantherophis guttatus lipa (SCG)
94
Eublepharis macularius lipa (SCG, SK)
98 Opheodrys aestivus lipa (SCG)
95
Pantherophis guttatus lip (SAL)
91 Echis coloratus lipa-b (VG, SCG)
96 64
Python regius lipa-b (SCG)
Anolis carolinensis lysosomal acid lipase/cholesteryl ester hydrolase [XP 003224417]
Python regius lipa (SCG)
Eublepharis macularius lipa (SCG)
100 Eublepharis macularius lipa (SAL)
Eublepharis macularius lipa (SK)
99 Pantherophis guttatus lipa (SCG)
Python regius lipa (SK)
62 Monodelphis domestica LIPA [ENSMODG00000019646]
98 Homo sapiens lysosomal acid lipase [AAB60328]
99 Mus musculus lysosomal acid lipase/cholesteryl ester hydrolase [NP 067435]
Rattus norvegicus lysosomal acid lipase/cholesteryl ester hydrolase [NP 036864]
Xenopus tropicalis lysosomal acid lipase/cholesteryl ester hydrolase [NP001015847]
Latimeria chalumnae LIPA [ENSLACG00000000424]
0.1

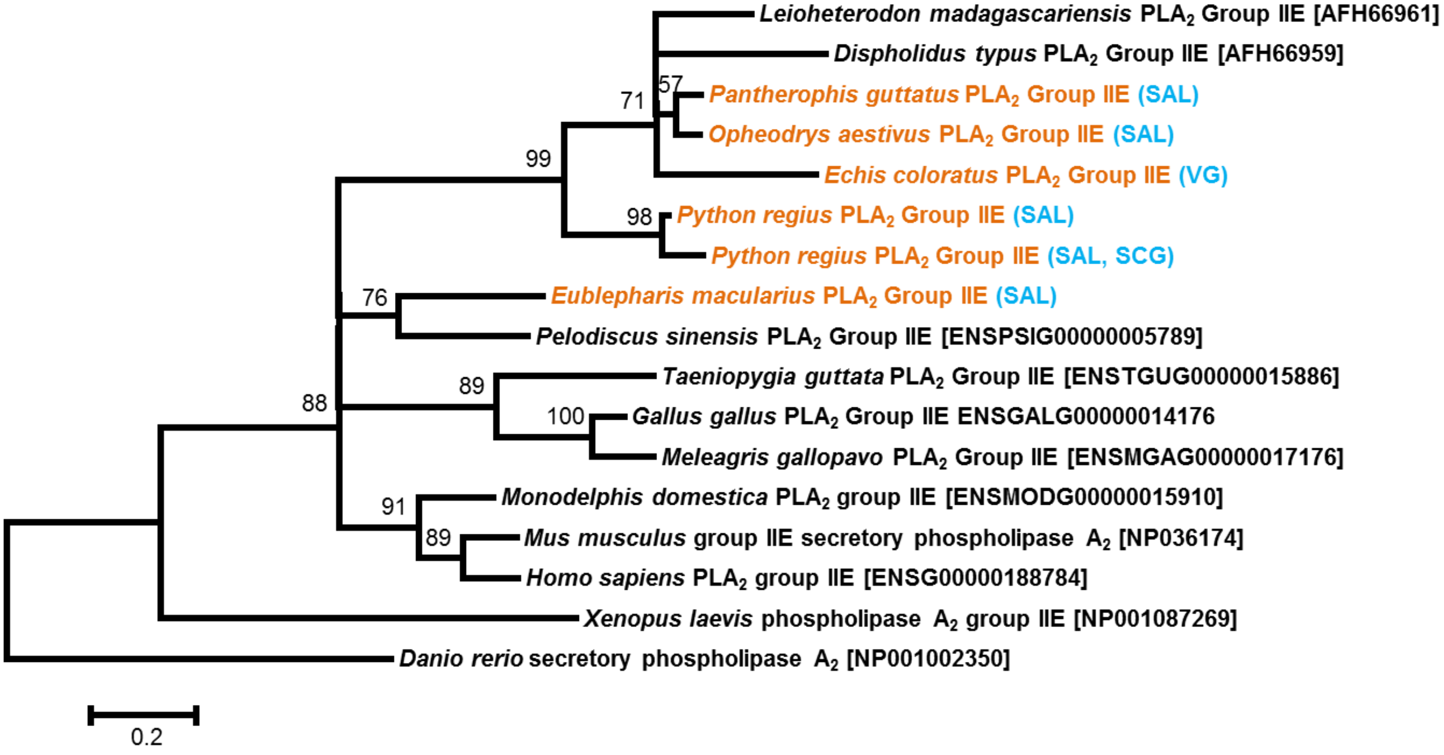
Supplementary figure S8

Maximum likelihood tree of *lysosomal acid lipase* (*lipa*) sequences. Genbank accession numbers or Ensembl gene IDs are given in square brackets. Sequences from this study are in orange text and the location of transcripts is provided in bracketed blue text (VG, venom gland; SAL, salivary gland; SK, skin; SCG, scent gland). Numbers above branches correspond to Bootstrap values for 500 replicates.


Bungarus multicinctus NGF [AAB25729]
Drysdalia coronoides NGF [AEH95535]
Denisonia devisi NGF-Den-2 [JAA74726]
Ophiophagus hannah ngf (VG)
Ophiophagus hannah ngf (Genomic- scaffold12849.1)
60
Naja sputatrix NGF [Q5YF89]
73
Naja naja Venom nerve growth factor [P01140]
Naja kaouthia nerve growth factor [A59218]
Naja atra Venom nerve growth factor [P61898]
Walterinnesia aegyptia venom nerve growth factor [AEH59581]
Micrurus fulvius NGF-1a (VG)
53
Micrurus fulvius NGF-1b (VG)
*
Naja sputatrix NGF [AAS94268]
Naja kaouthia nerve growth factor beta polypeptide [ACC85831]
Ophiophagus hannah hypothetical protein L345 10532 [ETE63701]
Ophiophagus hannah ngf (Genomic- scaffold2616.1)
Laticauda colubrina nerve growth factor beta polypeptide [ACC85824]
Pseudonaja textilis NGF [Q3HXY9]
Oxyuranus microlepidotus NGF [ABA60117]
Trimeresurus flavoviridis NGF [BAG16511]
75
Lachesis stenophrys nerve growth factor beta polypeptide [ACC85821]
Ovophis okinavensis NGF [BAN82142]
Crotalus durissus NGF [Q9DEZ9]
Bothrops jararacussu NGF [AAG12169]
79
Bothrops asper nerve growth factor beta polypeptide [ACC85807]
Macrovipera lebetina NGF [P25428]
Daboia russelii nerve growth factor beta polypeptide [ACC85813]
Echis coloratus ngf (VG, SCG, SK)
Azemiops feae NGF-AZE1 [AAZ75635]
94
Thamnophis marcianus nerve growth factor beta polypeptide [ACC85837]
Opheodrys aestivus ngf (SCG, SK)
76
Pantherophis guttatus ngf (SAL, SCG)
Lampropeltis getula nerve growth factor beta polypeptide [ACC85822]
Python regius ngf (SK)
Python molurus ngf [AEQU010205372] (Genomic- Contig26560677)
50
Boa constrictor nerve growth factor beta polypeptide [ACC85806]
Anolis carolinensis ngf [ENSACAP00000003352]
Varanus acanthurus NGF-VAR1 [AAZ75634]
Varanus salvator nerve growth factor beta polypeptide [ACC85794]
Eublepharis macularius ngf (SAL, SCG, SK)
99
Taeniopygia guttata NGF [ENSTGUG00000000958]
100
Gallus gallus NGF [ENSGALG00000002556]
Meleagris gallopavo [NGFENSMGAG00000015674]
93
Monodelphis domestica NGF [ENSMODG00000004863]
100
Homo sapiens NGF [ENSG00000134259]
100
Mus musculus NGF [AAA37686]
Rattus norvegicus NGF [ENSRNOG00000016571]
Latimeria chalumnae NGF [ENSLACG00000018594]
0.1

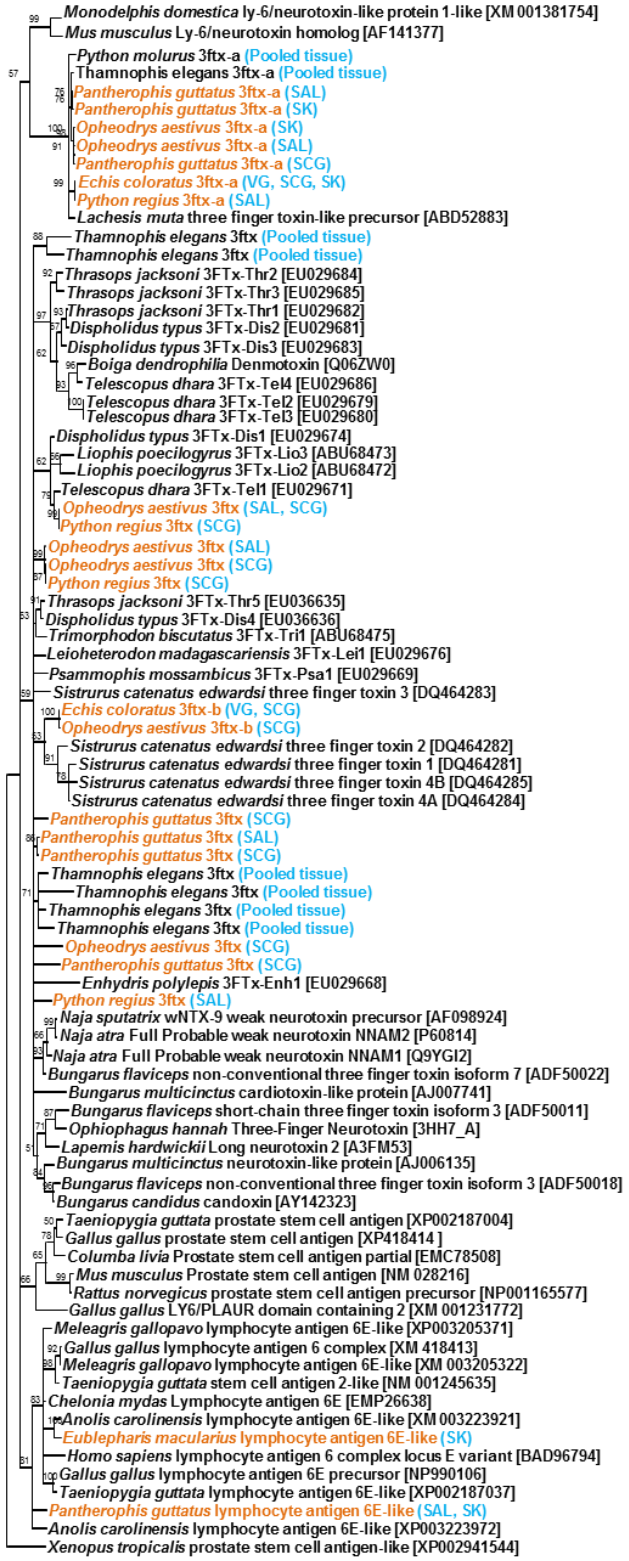
Supplementary figure S9

Maximum likelihood tree of *nerve growth factor* (*ngf*) sequences. Genbank accession numbers or Ensembl gene IDs are given in square brackets. Sequences from this study are in orange text and the location of transcripts is provided in bracketed blue text (VG, venom gland; SAL, salivary gland; SK, skin; SCG, scent gland). Numbers above branches correspond to Bootstrap values for 500 replicates.


Leioheterodon madagascariensis PLA$_2$ Group IIE [AFH66961]
Dispholidus typus PLA$_2$ Group IIE [AFH66959]
57
71
Pantherophis guttatus PLA$_2$ Group IIE (SAL)
Opheodrys aestivus PLA$_2$ Group IIE (SAL)
99
Echis coloratus PLA$_2$ Group IIE (VG)
98
Python regius PLA$_2$ Group IIE (SAL)
Python regius PLA$_2$ Group IIE (SAL, SCG)
76
Eublepharis macularius PLA$_2$ Group IIE (SAL)
Pelodiscus sinensis PLA$_2$ Group IIE [ENSPSIG00000005789]
89
Taeniopygia guttata PLA$_2$ Group IIE [ENSTGUG00000015886]
88
100
Gallus gallus PLA$_2$ Group IIE ENSGALG00000014176
Meleagris gallopavo PLA$_2$ Group IIE [ENSMGAG00000017176]
91
Monodelphis domestica PLA$_2$ group IIE [ENSMODG00000015910]
89
Mus musculus group IIE secretory phospholipase A$_2$ [NP036174]
Homo sapiens PLA$_2$ group IIE [ENSG00000188784]
Xenopus laevis phospholipase A$_2$ group IIE [NP001087269]
Danio rerio secretory phospholipase A$_2$ [NP001002350]
0.2

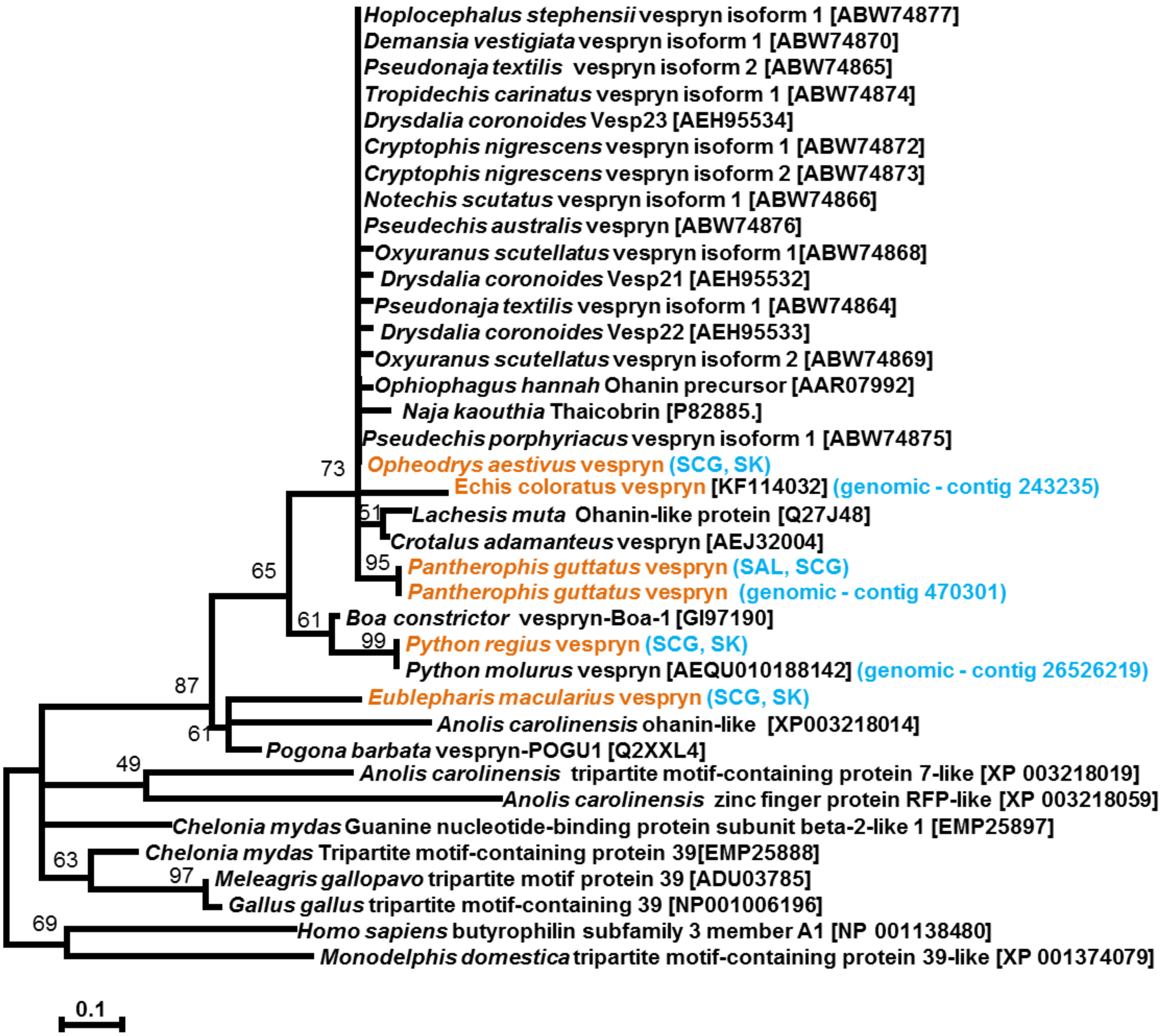
Supplementary figure S10

Maximum likelihood tree of *Group IIE Phospholipase A_2* (*PLA_2 Group IIE*) sequences. Genbank accession numbers or Ensembl gene IDs are given in square brackets. Sequences from this study are in orange text and the location of transcripts is provided in bracketed blue text (VG, venom gland; SAL, salivary gland; SK, skin; SCG, scent gland). Numbers above branches correspond to Bootstrap values for 500 replicates.


Monodelphis domestica ly-6/neurotoxin-like protein 1-like [XM 001381754]
Mus musculus Ly-6/neurotoxin homolog [AF141377]
Python molurus 3ftx-a (Pooled tissue)
Thamnophis elegans 3ftx-a (Pooled tissue)
Pantherophis guttatus 3ftx-a (SAL)
Pantherophis guttatus 3ftx-a (SK)
Opheodrys aestivus 3ftx-a (SK)
Opheodrys aestivus 3ftx-a (SAL)
Pantherophis guttatus 3ftx-a (SCG)
Echis coloratus 3ftx-a (VG, SCG, SK)
Python regius 3ftx-a (SAL)
Lachesis muta three finger toxin-like precursor [ABD52883]
Thamnophis elegans 3ftx (Pooled tissue)
Thamnophis elegans 3ftx (Pooled tissue)
Thrasops jacksoni 3FTx-Thr2 [EU029684]
Thrasops jacksoni 3FTx-Thr3 [EU029685]
Thrasops jacksoni 3FTx-Thr1 [EU029682]
Dispholidus typus 3FTx-Dis2 [EU029681]
Dispholidus typus 3FTx-Dis3 [EU029683]
Boiga dendrophilia Denmotoxin [Q06ZW0]
Telescopus dhara 3FTx-Tel4 [EU029686]
Telescopus dhara 3FTx-Tel2 [EU029679]
Telescopus dhara 3FTx-Tel3 [EU029680]
Dispholidus typus 3FTx-Dis1 [EU029674]
Liophis poecilogyrus 3FTx-Lio3 [ABU68473]
Liophis poecilogyrus 3FTx-Lio2 [ABU68472]
Telescopus dhara 3FTx-Tel1 [EU029671]
Opheodrys aestivus 3ftx (SAL, SCG)
Python regius 3ftx (SCG)
Opheodrys aestivus 3ftx (SAL)
Opheodrys aestivus 3ftx (SCG)
Python regius 3ftx (SCG)
Thrasops jacksoni 3FTx-Thr5 [EU036635]
Dispholidus typus 3FTx-Dis4 [EU036636]
Trimorphodon biscutatus 3FTx-Tri1 [ABU68475]
Leioheterodon madagascariensis 3FTx-Lei1 [EU029676]
Psammophis mossambicus 3FTx-Psa1 [EU029669]
Sistrurus catenatus edwardsi three finger toxin 3 [DQ464283]
Echis coloratus 3ftx-b (VG, SCG)
Opheodrys aestivus 3ftx-b (SCG)
Sistrurus catenatus edwardsi three finger toxin 2 [DQ464282]
Sistrurus catenatus edwardsi three finger toxin 1 [DQ464281]
Sistrurus catenatus edwardsi three finger toxin 4B [DQ464285]
Sistrurus catenatus edwardsi three finger toxin 4A [DQ464284]
Pantherophis guttatus 3ftx (SCG)
Pantherophis guttatus 3ftx (SAL)
Pantherophis guttatus 3ftx (SCG)
Thamnophis elegans 3ftx (Pooled tissue)
Thamnophis elegans 3ftx (Pooled tissue)
Thamnophis elegans 3ftx (Pooled tissue)
Thamnophis elegans 3ftx (Pooled tissue)
Opheodrys aestivus 3ftx (SCG)
Pantherophis guttatus 3ftx (SCG)
Enhydris polylepis 3FTx-Enh1 [EU029668]
Python regius 3ftx (SAL)
Naja sputatrix wNTX-9 weak neurotoxin precursor [AF098924]
Naja atra Full Probable weak neurotoxin NNAM2 [P60814]
Naja atra Full Probable weak neurotoxin NNAM1 [Q9YGI2]
Bungarus flaviceps non-conventional three finger toxin isoform 7 [ADF50022]
Bungarus multicinctus cardiotoxin-like protein [AJ007741]
Bungarus flaviceps short-chain three finger toxin isoform 3 [ADF50011]
Ophiophagus hannah Three-Finger Neurotoxin [3HH7_A]
Lapemis hardwickii Long neurotoxin 2 [A3FM53]
Bungarus multicinctus neurotoxin-like protein [AJ006135]
Bungarus flaviceps non-conventional three finger toxin isoform 3 [ADF50018]
Bungarus candidus candoxin [AY142323]
Taeniopygia guttata prostate stem cell antigen [XP002187004]
Gallus gallus prostate stem cell antigen [XP418414]
Columba livia Prostate stem cell antigen partial [EMC78508]
Mus musculus Prostate stem cell antigen [NM 028216]
Rattus norvegicus prostate stem cell antigen precursor [NP001165577]
Gallus gallus LY6/PLAUR domain containing 2 [XM 001231772]
Meleagris gallopavo lymphocyte antigen 6E-like [XP003205371]
Gallus gallus lymphocyte antigen 6 complex [XM 418413]
Meleagris gallopavo lymphocyte antigen 6E-like [XM 003205322]
Taeniopygia guttata stem cell antigen 2-like [NM 001245635]
Chelonia mydas Lymphocyte antigen 6E [EMP26638]
Anolis carolinensis lymphocyte antigen 6E-like [XM 003223921]
Eublepharis macularius lymphocyte antigen 6E-like (SK)
Homo sapiens lymphocyte antigen 6 complex locus E variant [BAD96794]
Gallus gallus lymphocyte antigen 6E precursor [NP990106]
Taeniopygia guttata lymphocyte antigen 6E-like [XP002187037]
Pantherophis guttatus lymphocyte antigen 6E-like (SAL, SK)
Anolis carolinensis lymphocyte antigen 6E-like [XP003223972]
Xenopus tropicalis prostate stem cell antigen-like [XP002941544]

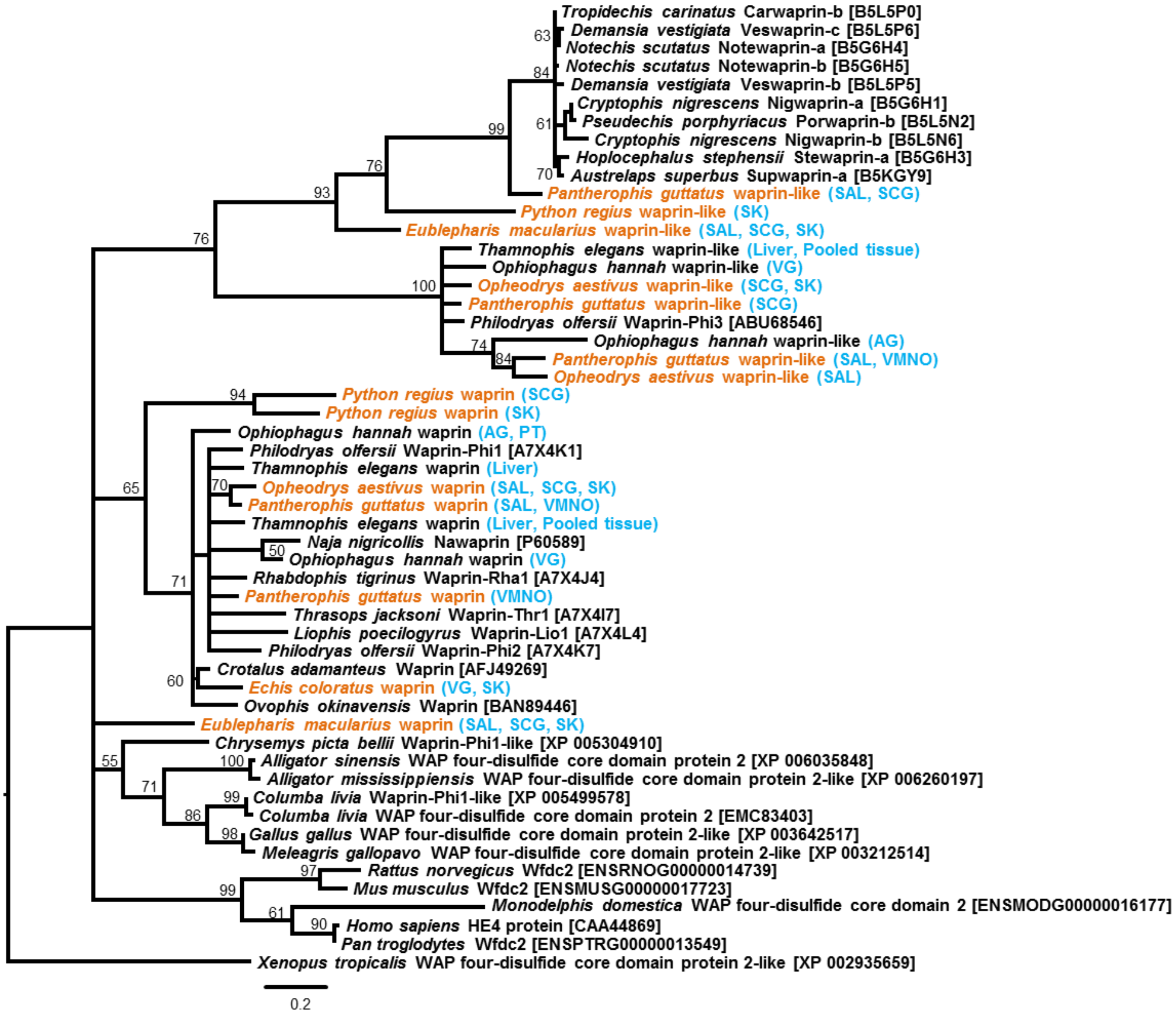
Supplementary figure S11

Maximum likelihood tree of *three finger toxin (3ftx)* genes. Genbank accession numbers or Ensembl gene IDs are given in square brackets. Sequences from this study are in orange text and the location of transcripts is provided in bracketed blue text (VG, venom gland; SAL, salivary gland; SK, skin; SCG, scent gland). Numbers above branches correspond to Bootstrap values for 500 replicates.


Hoplocephalus stephensii vespryn isoform 1 [ABW74877]
Demansia vestigiata vespryn isoform 1 [ABW74870]
Pseudonaja textilis vespryn isoform 2 [ABW74865]
Tropidechis carinatus vespryn isoform 1 [ABW74874]
Drysdalia coronoides Vesp23 [AEH95534]
Cryptophis nigrescens vespryn isoform 1 [ABW74872]
Cryptophis nigrescens vespryn isoform 2 [ABW74873]
Notechis scutatus vespryn isoform 1 [ABW74866]
Pseudechis australis vespryn [ABW74876]
Oxyuranus scutellatus vespryn isoform 1[ABW74868]
Drysdalia coronoides Vesp21 [AEH95532]
Pseudonaja textilis vespryn isoform 1 [ABW74864]
Drysdalia coronoides Vesp22 [AEH95533]
Oxyuranus scutellatus vespryn isoform 2 [ABW74869]
Ophiophagus hannah Ohanin precursor [AAR07992]
Naja kaouthia Thaicobrin [P82885.]
Pseudechis porphyriacus vespryn isoform 1 [ABW74875]
73
Opheodrys aestivus vespryn (SCG, SK)
Echis coloratus vespryn [KF114032] (genomic - contig 243235)
51
Lachesis muta Ohanin-like protein [Q27J48]
Crotalus adamanteus vespryn [AEJ32004]
65
95
Pantherophis guttatus vespryn (SAL, SCG)
Pantherophis guttatus vespryn (genomic - contig 470301)
61
Boa constrictor vespryn-Boa-1 [GI97190]
99
Python regius vespryn (SCG, SK)
Python molurus vespryn [AEQU010188142] (genomic - contig 26526219)
87
Eublepharis macularius vespryn (SCG, SK)
Anolis carolinensis ohanin-like [XP003218014]
61
Pogona barbata vespryn-POGU1 [Q2XXL4]
49
Anolis carolinensis tripartite motif-containing protein 7-like [XP 003218019]
Anolis carolinensis zinc finger protein RFP-like [XP 003218059]
Chelonia mydas Guanine nucleotide-binding protein subunit beta-2-like 1 [EMP25897]
63
Chelonia mydas Tripartite motif-containing protein 39[EMP25888]
97
Meleagris gallopavo tripartite motif protein 39 [ADU03785]
Gallus gallus tripartite motif-containing 39 [NP001006196]
69
Homo sapiens butyrophilin subfamily 3 member A1 [NP 001138480]
Monodelphis domestica tripartite motif-containing protein 39-like [XP 001374079]
0.1

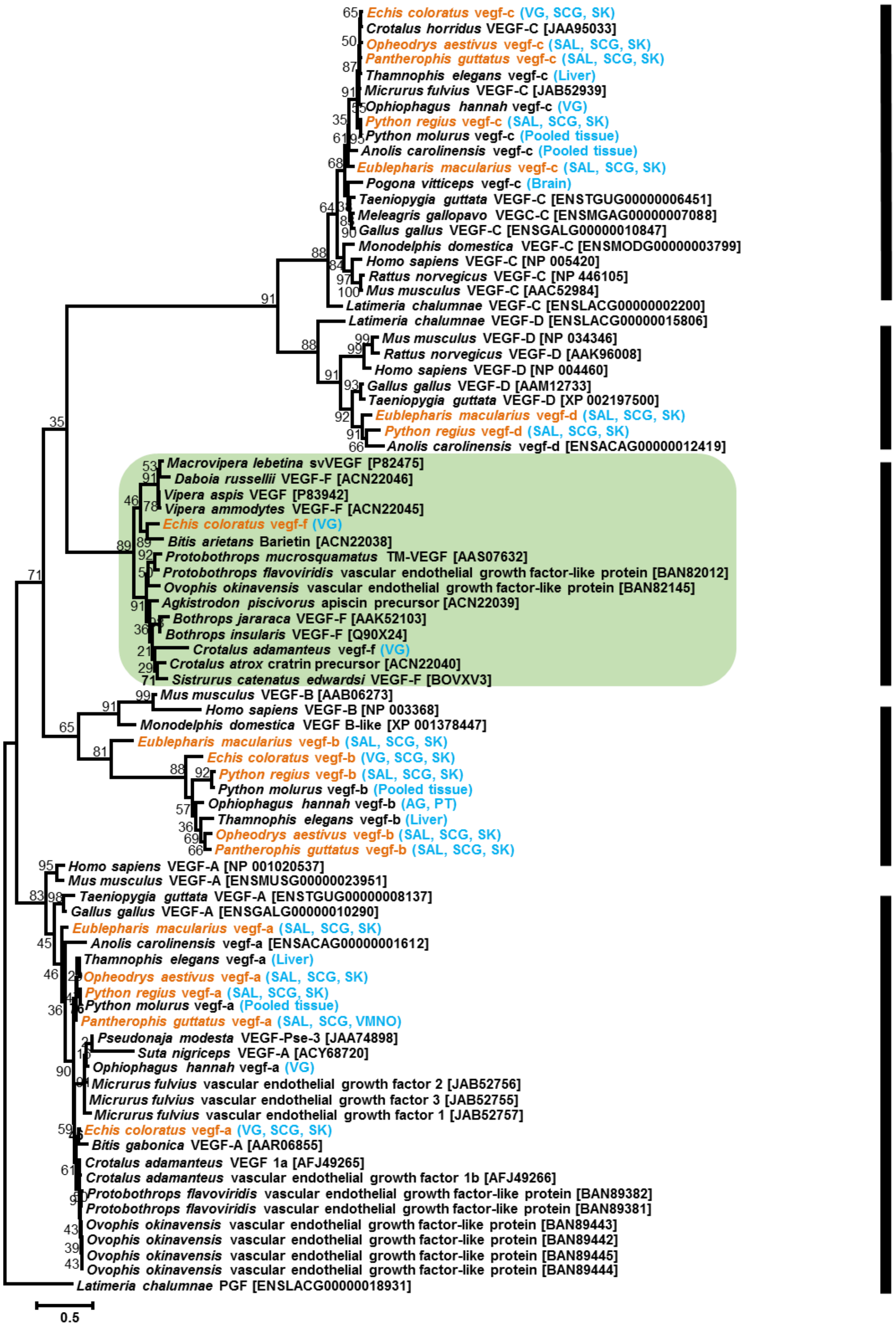
Supplementary figure S12

Maximum likelihood tree of *vespryn* sequences. Genbank accession numbers are given in square brackets. Sequences from this study are in orange text and the location of transcripts is provided in bracketed blue text (VG, venom gland; SAL, salivary gland; SK, skin; SCG, scent gland). Numbers above branches correspond to Bootstrap values for 500 replicates.

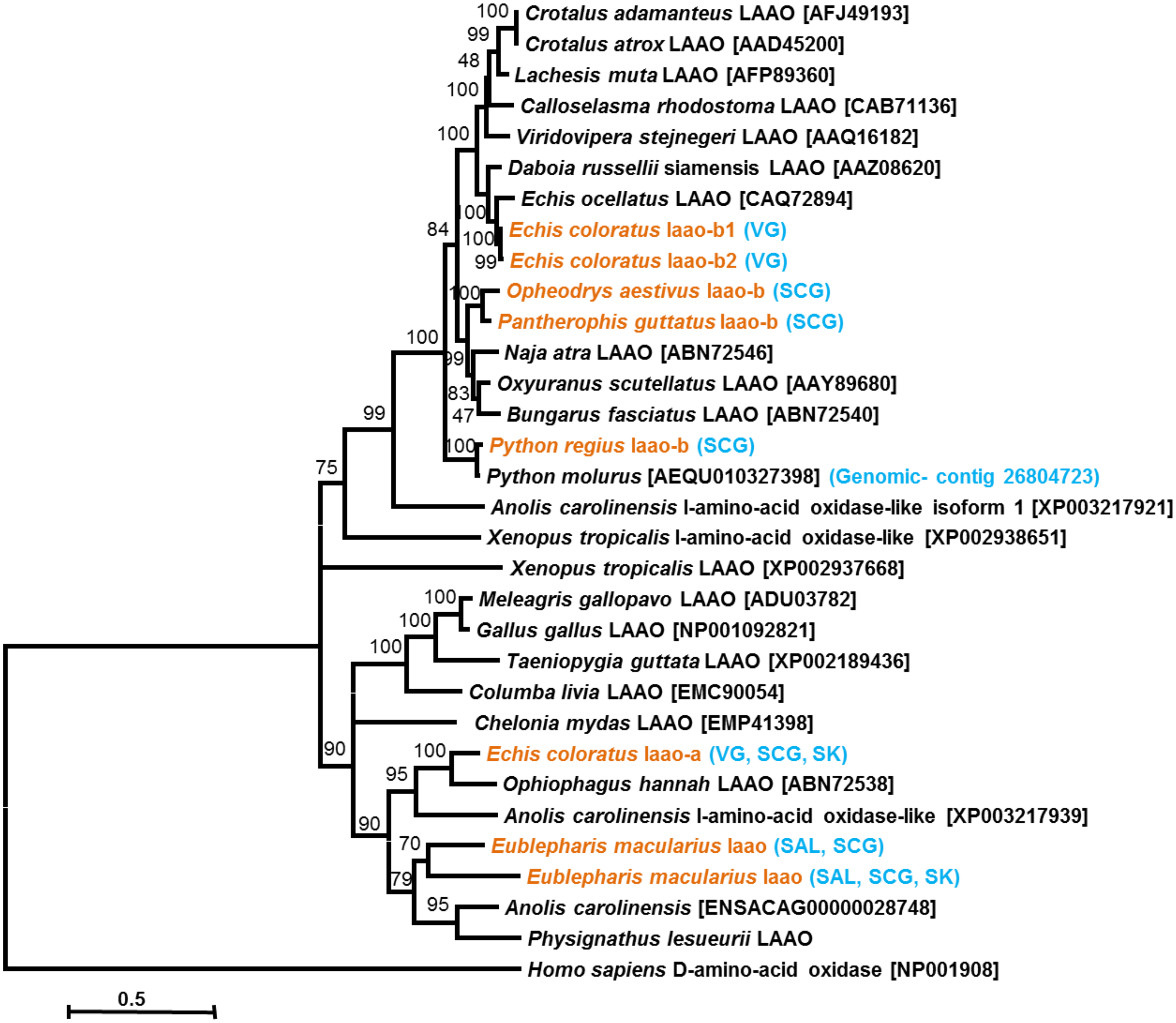

Tropidechis carinatus Carwaprin-b [B5L5P0]
63
Demansia vestigiata Veswaprin-c [B5L5P6]
Notechis scutatus Notewaprin-a [B5G6H4]
84
Notechis scutatus Notewaprin-b [B5G6H5]
Demansia vestigiata Veswaprin-b [B5L5P5]
Cryptophis nigrescens Nigwaprin-a [B5G6H1]
61
Pseudechis porphyriacus Porwaprin-b [B5L5N2]
99
Cryptophis nigrescens Nigwaprin-b [B5L5N6]
Hoplocephalus stephensii Stewaprin-a [B5G6H3]
76
70
Austrelaps superbus Supwaprin-a [B5KGY9]
93
Pantherophis guttatus waprin-like (SAL, SCG)
Python regius waprin-like (SK)
Eublepharis macularius waprin-like (SAL, SCG, SK)
76
Thamnophis elegans waprin-like (Liver, Pooled tissue)
Ophiophagus hannah waprin-like (VG)
100
Opheodrys aestivus waprin-like (SCG, SK)
Pantherophis guttatus waprin-like (SCG)
Philodryas olfersii Waprin-Phi3 [ABU68546]
74
Ophiophagus hannah waprin-like (AG)
84
Pantherophis guttatus waprin-like (SAL, VMNO)
Opheodrys aestivus waprin-like (SAL)
94
Python regius waprin (SCG)
Python regius waprin (SK)
Ophiophagus hannah waprin (AG, PT)
Philodryas olfersii Waprin-Phi1 [A7X4K1]
Thamnophis elegans waprin (Liver)
70
Opheodrys aestivus waprin (SAL, SCG, SK)
65
Pantherophis guttatus waprin (SAL, VMNO)
Thamnophis elegans waprin (Liver, Pooled tissue)
Naja nigricollis Nawaprin [P60589]
50
Ophiophagus hannah waprin (VG)
71
Rhabdophis tigrinus Waprin-Rha1 [A7X4J4]
Pantherophis guttatus waprin (VMNO)
Thrasops jacksoni Waprin-Thr1 [A7X4I7]
Liophis poecilogyrus Waprin-Lio1 [A7X4L4]
Philodryas olfersii Waprin-Phi2 [A7X4K7]
Crotalus adamanteus Waprin [AFJ49269]
60
Echis coloratus waprin (VG, SK)
Ovophis okinavensis Waprin [BAN89446]
Eublepharis macularius waprin (SAL, SCG, SK)
Chrysemys picta bellii Waprin-Phi1-like [XP 005304910]
55
100
Alligator sinensis WAP four-disulfide core domain protein 2 [XP 006035848]
71
Alligator mississippiensis WAP four-disulfide core domain protein 2-like [XP 006260197]
99
Columba livia Waprin-Phi1-like [XP 005499578]
86
Columba livia WAP four-disulfide core domain protein 2 [EMC83403]
98
Gallus gallus WAP four-disulfide core domain protein 2-like [XP 003642517]
Meleagris gallopavo WAP four-disulfide core domain protein 2-like [XP 003212514]
97
Rattus norvegicus Wfdc2 [ENSRNOG00000014739]
99
Mus musculus Wfdc2 [ENSMUSG00000017723]
Monodelphis domestica WAP four-disulfide core domain 2 [ENSMODG00000016177]
61
90
Homo sapiens HE4 protein [CAA44869]
Pan troglodytes Wfdc2 [ENSPTRG00000013549]
Xenopus tropicalis WAP four-disulfide core domain protein 2-like [XP 002935659]
0.2

Supplementary figure S13

Maximum likelihood tree of *waprin* sequences. Genbank accession numbers or Ensembl gene IDs are given in square brackets. Sequences from this study are in orange text and the location of transcripts is provided in bracketed blue text (VG, venom gland; SAL, salivary gland; SK, skin; SCG, scent gland; AG, accessory gland; PT, pooled tissue; VMNO, vomeronasal organ). Numbers above branches correspond to Bootstrap values for 500 replicates. The two *Echis coloratus* sequences are likely to be alleles or the result of variation in the two individuals used to generate the transcriptomes.


65 Echis coloratus vegf-c (VG, SCG, SK)
Crotalus horridus VEGF-C [JAA95033]
50 Opheodrys aestivus vegf-c (SAL, SCG, SK)
Pantherophis guttatus vegf-c (SAL, SCG, SK)
87 Thamnophis elegans vegf-c (Liver)
91 Micrurus fulvius VEGF-C [JAB52939]
Ophiophagus hannah vegf-c (VG)
35 Python regius vegf-c (SAL, SCG, SK)
61 95 Python molurus vegf-c (Pooled tissue)
Anolis carolinensis vegf-c (Pooled tissue)
68 Eublepharis macularius vegf-c (SAL, SCG, SK)
Pogona vitticeps vegf-c (Brain)
Taeniopygia guttata VEGF-C [ENSTGUG00000006451]
64 Meleagris gallopavo VEGC-C [ENSMGAG00000007088]
90 Gallus gallus VEGF-C [ENSGALG00000010847]
Monodelphis domestica VEGF-C [ENSMODG00000003799]
88 84 Homo sapiens VEGF-C [NP 005420]
97 Rattus norvegicus VEGF-C [NP 446105]
100 Mus musculus VEGF-C [AAC52984]
91 Latimeria chalumnae VEGF-C [ENSLACG00000002200]
Latimeria chalumnae VEGF-D [ENSLACG00000015806]
99 Mus musculus VEGF-D [NP 034346]
88 99 Rattus norvegicus VEGF-D [AAK96008]
91 Homo sapiens VEGF-D [NP 004460]
93 Gallus gallus VEGF-D [AAM12733]
Taeniopygia guttata VEGF-D [XP 002197500]
92 Eublepharis macularius vegf-d (SAL, SCG, SK)
91 Python regius vegf-d (SAL, SCG, SK)
35 66 Anolis carolinensis vegf-d [ENSACAG00000012419]
53 Macrovipera lebetina svVEGF [P82475]
91 Daboia russellii VEGF-F [ACN22046]
46 Vipera aspis VEGF [P83942]
78 Vipera ammodytes VEGF-F [ACN22045]
Echis coloratus vegf-f (VG)
89 89 Bitis arietans Barietin [ACN22038]
92 Protobothrops mucrosquamatus TM-VEGF [AAS07632]
Protobothrops flavoviridis vascular endothelial growth factor-like protein [BAN82012]
71 Ovophis okinavensis vascular endothelial growth factor-like protein [BAN82145]
91 Agkistrodon piscivorus apiscin precursor [ACN22039]
Bothrops jararaca VEGF-F [AAK52103]
36 Bothrops insularis VEGF-F [Q90X24]
21 Crotalus adamanteus vegf-f (VG)
29 Crotalus atrox cratrin precursor [ACN22040]
71 Sistrurus catenatus edwardsi VEGF-F [BOVXV3]
99 Mus musculus VEGF-B [AAB06273]
91 Homo sapiens VEGF-B [NP 003368]
65 Monodelphis domestica VEGF B-like [XP 001378447]
Eublepharis macularius vegf-b (SAL, SCG, SK)
81 Echis coloratus vegf-b (VG, SCG, SK)
88 92 Python regius vegf-b (SAL, SCG, SK)
Python molurus vegf-b (Pooled tissue)
57 Ophiophagus hannah vegf-b (AG, PT)
Thamnophis elegans vegf-b (Liver)
36 69 Opheodrys aestivus vegf-b (SAL, SCG, SK)
66 Pantherophis guttatus vegf-b (SAL, SCG, SK)
95 Homo sapiens VEGF-A [NP 001020537]
Mus musculus VEGF-A [ENSMUSG00000023951]
83 98 Taeniopygia guttata VEGF-A [ENSTGUG00000008137]
Gallus gallus VEGF-A [ENSGALG00000010290]
Eublepharis macularius vegf-a (SAL, SCG, SK)
45 Anolis carolinensis vegf-a [ENSACAG00000001612]
Thamnophis elegans vegf-a (Liver)
46 Opheodrys aestivus vegf-a (SAL, SCG, SK)
Python regius vegf-a (SAL, SCG, SK)
36 Python molurus vegf-a (Pooled tissue)
Pantherophis guttatus vegf-a (SAL, SCG, VMNO)
Pseudonaja modesta VEGF-Pse-3 [JAA74898]
Suta nigriceps VEGF-A [ACY68720]
90 Ophiophagus hannah vegf-a (VG)
Micrurus fulvius vascular endothelial growth factor 2 [JAB52756]
Micrurus fulvius vascular endothelial growth factor 3 [JAB52755]
Micrurus fulvius vascular endothelial growth factor 1 [JAB52757]
59 Echis coloratus vegf-a (VG, SCG, SK)
Bitis gabonica VEGF-A [AAR06855]
61 Crotalus adamanteus VEGF 1a [AFJ49265]
Crotalus adamanteus vascular endothelial growth factor 1b [AFJ49266]
Protobothrops flavoviridis vascular endothelial growth factor-like protein [BAN89382]
Protobothrops flavoviridis vascular endothelial growth factor-like protein [BAN89381]
43 Ovophis okinavensis vascular endothelial growth factor-like protein [BAN89443]
Ovophis okinavensis vascular endothelial growth factor-like protein [BAN89442]
39 Ovophis okinavensis vascular endothelial growth factor-like protein [BAN89445]
43 Ovophis okinavensis vascular endothelial growth factor-like protein [BAN89444]
71 Latimeria chalumnae PGF [ENSLACG00000018931]
0.5
C
D
F
B
A

Supplementary figure S14
Maximum likelihood tree of *vascular endothelial growth factor* (*vegf*) sequences. Monophyletic clades representing the five members of the *vegf* family (*a-f*) are indicated and the putative viper venom-specific *vegf-f* clade is shaded green. Genbank accession numbers or Ensembl gene IDs are given in square brackets. Sequences from this study are in orange text and the location of transcripts is provided in bracketed blue text (VG, venom gland; SAL, salivary gland; SK, skin; SCG, scent gland; AG, accessory gland; PT, pooled tissue; VMNO, vomeronasal organ). Numbers above branches correspond to Bootstrap values for 500 replicates.


100
99
48
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83
47
100
100
99
75
Crotalus adamanteus LAAO [AFJ49193]
Crotalus atrox LAAO [AAD45200]
Lachesis muta LAAO [AFP89360]
Calloselasma rhodostoma LAAO [CAB71136]
Viridovipera stejnegeri LAAO [AAQ16182]
Daboia russellii siamensis LAAO [AAZ08620]
Echis ocellatus LAAO [CAQ72894]
Echis coloratus laao-b1 (VG)
Echis coloratus laao-b2 (VG)
Opheodrys aestivus laao-b (SCG)
Pantherophis guttatus laao-b (SCG)
Naja atra LAAO [ABN72546]
Oxyuranus scutellatus LAAO [AAY89680]
Bungarus fasciatus LAAO [ABN72540]
Python regius laao-b (SCG)
Python molurus [AEQU010327398] (Genomic- contig 26804723)
Anolis carolinensis l-amino-acid oxidase-like isoform 1 [XP003217921]
Xenopus tropicalis l-amino-acid oxidase-like [XP002938651]
Xenopus tropicalis LAAO [XP002937668]
100
100
100
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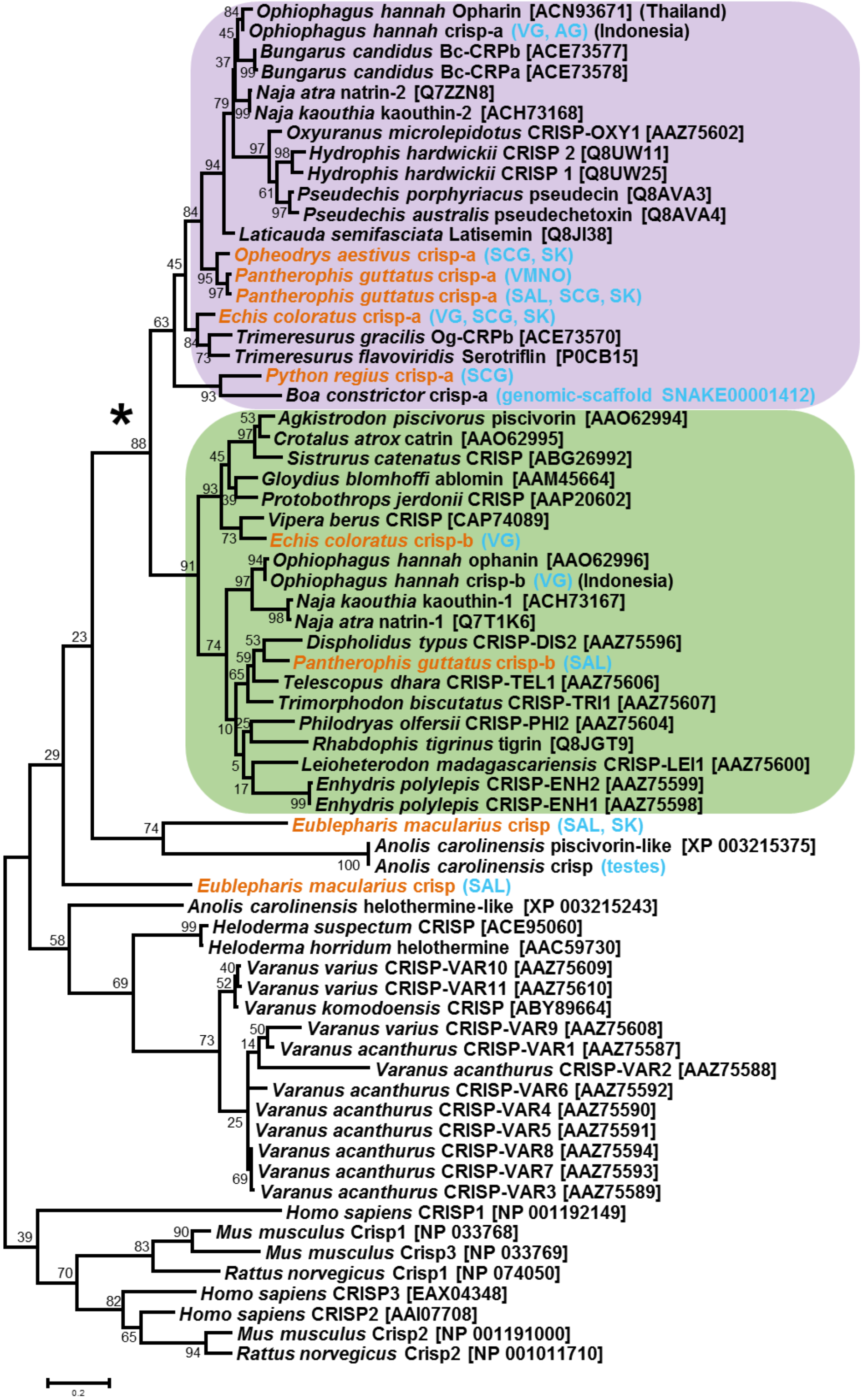
100
95
90
70
79
95
Meleagris gallopavo LAAO [ADU03782]
Gallus gallus LAAO [NP001092821]
Taeniopygia guttata LAAO [XP002189436]
Columba livia LAAO [EMC90054]
Chelonia mydas LAAO [EMP41398]
Echis coloratus laao-a (VG, SCG, SK)
Ophiophagus hannah LAAO [ABN72538]
Anolis carolinensis l-amino-acid oxidase-like [XP003217939]
Eublepharis macularius laao (SAL, SCG)
Eublepharis macularius laao (SAL, SCG, SK)
Anolis carolinensis [ENSACAG00000028748]
Physignathus lesueurii LAAO
Homo sapiens D-amino-acid oxidase [NP001908]
0.5

Supplementary figure S15

Maximum likelihood tree of *l-amino acid oxidase* (*laao*) sequences. Genbank accession numbers or Ensembl gene IDs are given in square brackets (the Australian Water Dragon (*Physignathus lesueurii*) sequence does not have a Genbank accession number and is derived from a sequence in [2]). Sequences from this study are in orange text and the location of transcripts is provided in bracketed blue text (VG, venom gland; SAL, salivary gland; SK, skin; SCG, scent gland). Numbers above branches correspond to Bootstrap values for 500 replicates.


Ophiophagus hannah Opharin [ACN93671] (Thailand)
Ophiophagus hannah crisp-a (VG, AG) (Indonesia)
Bungarus candidus Bc-CRPb [ACE73577]
Bungarus candidus Bc-CRPa [ACE73578]
Naja atra natrin-2 [Q7ZZN8]
Naja kaouthia kaouthin-2 [ACH73168]
Oxyuranus microlepidotus CRISP-OXY1 [AAZ75602]
Hydrophis hardwickii CRISP 2 [Q8UW11]
Hydrophis hardwickii CRISP 1 [Q8UW25]
Pseudechis porphyriacus pseudecin [Q8AVA3]
Pseudechis australis pseudechetoxin [Q8AVA4]
Laticauda semifasciata Latisemin [Q8JI38]
Opheodrys aestivus crisp-a (SCG, SK)
Pantherophis guttatus crisp-a (VMNO)
Pantherophis guttatus crisp-a (SAL, SCG, SK)
Echis coloratus crisp-a (VG, SCG, SK)
Trimeresurus gracilis Og-CRPb [ACE73570]
Trimeresurus flavoviridis Serotriflin [P0CB15]
Python regius crisp-a (SCG)
Boa constrictor crisp-a (genomic-scaffold SNAKE00001412)
Agkistrodon piscivorus piscivorin [AAO62994]
Crotalus atrox catrin [AAO62995]
Sistrurus catenatus CRISP [ABG26992]
Gloydius blomhoffi ablomin [AAM45664]
Protobothrops jerdonii CRISP [AAP20602]
Vipera berus CRISP [CAP74089]
Echis coloratus crisp-b (VG)
Ophiophagus hannah ophanin [AAO62996]
Ophiophagus hannah crisp-b (VG) (Indonesia)
Naja kaouthia kaouthin-1 [ACH73167]
Naja atra natrin-1 [Q7T1K6]
Dispholidus typus CRISP-DIS2 [AAZ75596]
Pantherophis guttatus crisp-b (SAL)
Telescopus dhara CRISP-TEL1 [AAZ75606]
Trimorphodon biscutatus CRISP-TRI1 [AAZ75607]
Philodryas olfersii CRISP-PHI2 [AAZ75604]
Rhabdophis tigrinus tigrin [Q8JGT9]
Leioheterodon madagascariensis CRISP-LEI1 [AAZ75600]
Enhydris polylepis CRISP-ENH2 [AAZ75599]
Enhydris polylepis CRISP-ENH1 [AAZ75598]
Eublepharis macularius crisp (SAL, SK)
Anolis carolinensis piscivorin-like [XP 003215375]
Anolis carolinensis crisp (testes)
Eublepharis macularius crisp (SAL)
Anolis carolinensis helothermine-like [XP 003215243]
Heloderma suspectum CRISP [ACE95060]
Heloderma horridum helothermine [AAC59730]
Varanus varius CRISP-VAR10 [AAZ75609]
Varanus varius CRISP-VAR11 [AAZ75610]
Varanus komodoensis CRISP [ABY89664]
Varanus varius CRISP-VAR9 [AAZ75608]
Varanus acanthurus CRISP-VAR1 [AAZ75587]
Varanus acanthurus CRISP-VAR2 [AAZ75588]
Varanus acanthurus CRISP-VAR6 [AAZ75592]
Varanus acanthurus CRISP-VAR4 [AAZ75590]
Varanus acanthurus CRISP-VAR5 [AAZ75591]
Varanus acanthurus CRISP-VAR8 [AAZ75594]
Varanus acanthurus CRISP-VAR7 [AAZ75593]
Varanus acanthurus CRISP-VAR3 [AAZ75589]
Homo sapiens CRISP1 [NP 001192149]
Mus musculus Crisp1 [NP 033768]
Mus musculus Crisp3 [NP 033769]
Rattus norvegicus Crisp1 [NP 074050]
Homo sapiens CRISP3 [EAX04348]
Homo sapiens CRISP2 [AAI07708]
Mus musculus Crisp2 [NP 001191000]
Rattus norvegicus Crisp2 [NP 001011710]
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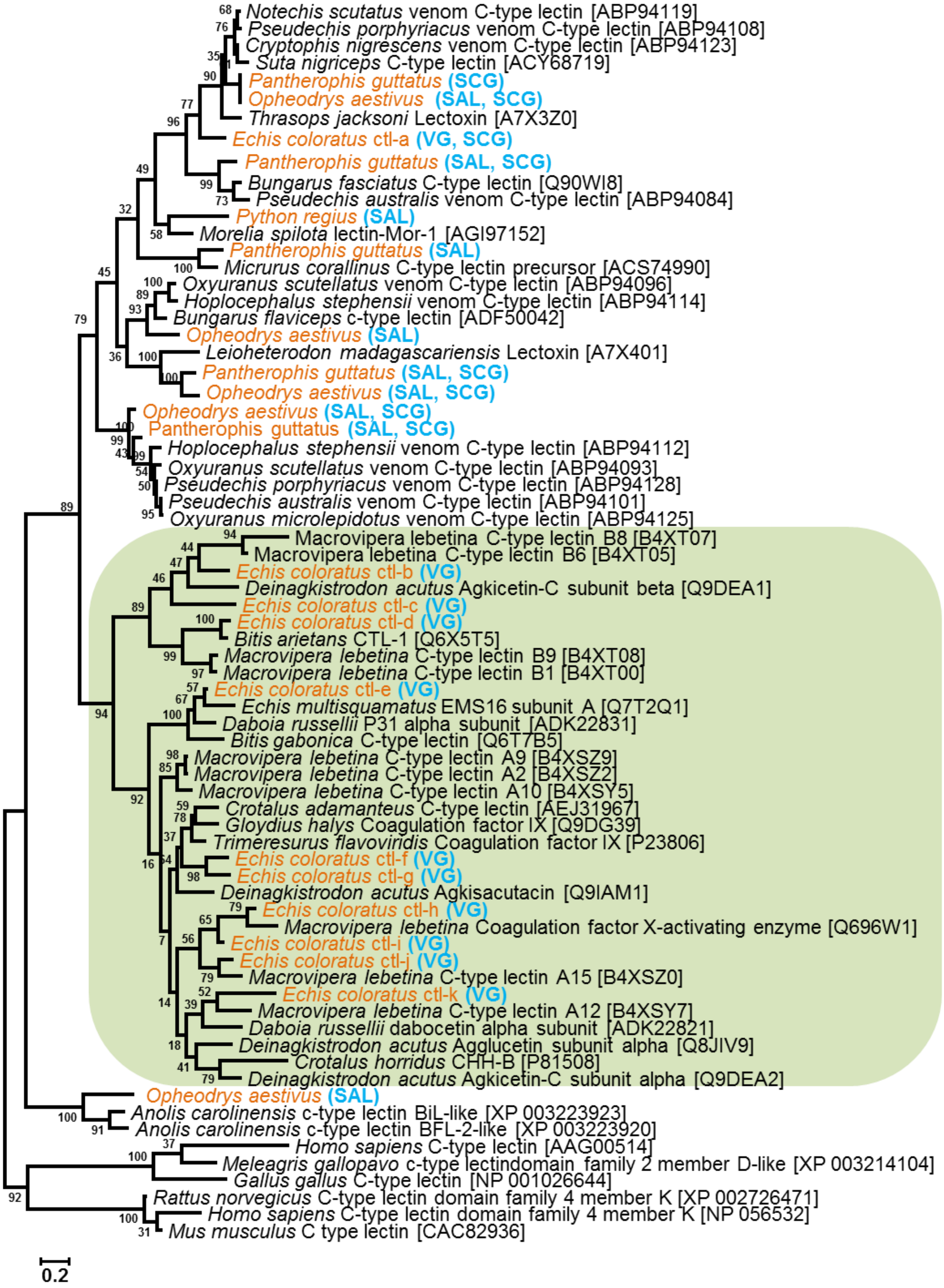
Supplementary figure S16

Maximum likelihood tree of *crisp* sequences. Genbank accession numbers are given in square brackets. Sequences from this study are in orange text and the location of transcripts is provided in bracketed blue text (VG, venom gland; SAL, salivary gland; SK, skin; SCG, scent gland; AG, accessory gland; VMNO, vomeronasal organ). Numbers above branches correspond to Bootstrap values for 500 replicates. The * denotes the gene duplication event that produced *crisp-a* (shaded purple) and *crisp-b* (green).


Notechis scutatus venom C-type lectin [ABP94119]
Pseudechis porphyriacus venom C-type lectin [ABP94108]
Cryptophis nigrescens venom C-type lectin [ABP94123]
Suta nigriceps C-type lectin [ACY68719]
Pantherophis guttatus (SCG)
Opheodrys aestivus (SAL, SCG)
Thrasops jacksoni Lectoxin [A7X3Z0]
Echis coloratus ctl-a (VG, SCG)
Pantherophis guttatus (SAL, SCG)
Bungarus fasciatus C-type lectin [Q90WI8]
Pseudechis australis venom C-type lectin [ABP94084]
Python regius (SAL)
Morelia spilota lectin-Mor-1 [AGI97152]
Pantherophis guttatus (SAL)
Micrurus corallinus C-type lectin precursor [ACS74990]
Oxyuranus scutellatus venom C-type lectin [ABP94096]
Hoplocephalus stephensii venom C-type lectin [ABP94114]
Bungarus flaviceps c-type lectin [ADF50042]
Opheodrys aestivus (SAL)
Leioheterodon madagascariensis Lectoxin [A7X401]
Pantherophis guttatus (SAL, SCG)
Opheodrys aestivus (SAL, SCG)
Opheodrys aestivus (SAL, SCG)
Pantherophis guttatus (SAL, SCG)
Hoplocephalus stephensii venom C-type lectin [ABP94112]
Oxyuranus scutellatus venom C-type lectin [ABP94093]
Pseudechis porphyriacus venom C-type lectin [ABP94128]
Pseudechis australis venom C-type lectin [ABP94101]
Oxyuranus microlepidotus venom C-type lectin [ABP94125]
Macrovipera lebetina C-type lectin B8 [B4XT07]
Macrovipera lebetina C-type lectin B6 [B4XT05]
Echis coloratus ctl-b (VG)
Deinagkistrodon acutus Agkicetin-C subunit beta [Q9DEA1]
Echis coloratus ctl-c (VG)
Echis coloratus ctl-d (VG)
Bitis arietans CTL-1 [Q6X5T5]
Macrovipera lebetina C-type lectin B9 [B4XT08]
Macrovipera lebetina C-type lectin B1 [B4XT00]
Echis coloratus ctl-e (VG)
Echis multisquamatus EMS16 subunit A [Q7T2Q1]
Daboia russellii P31 alpha subunit [ADK22831]
Bitis gabonica C-type lectin [Q6T7B5]
Macrovipera lebetina C-type lectin A9 [B4XSZ9]
Macrovipera lebetina C-type lectin A2 [B4XSZ2]
Macrovipera lebetina C-type lectin A10 [B4XSY5]
Crotalus adamanteus C-type lectin [AEJ31967]
Gloydius halys Coagulation factor IX [Q9DG39]
Trimeresurus flavoviridis Coagulation factor IX [P23806]
Echis coloratus ctl-f (VG)
Echis coloratus ctl-g (VG)
Deinagkistrodon acutus Agkisacutacin [Q9IAM1]
Echis coloratus ctl-h (VG)
Macrovipera lebetina Coagulation factor X-activating enzyme [Q696W1]
Echis coloratus ctl-i (VG)
Echis coloratus ctl-j (VG)
Macrovipera lebetina C-type lectin A15 [B4XSZ0]
Echis coloratus ctl-k (VG)
Macrovipera lebetina C-type lectin A12 [B4XSY7]
Daboia russellii dabocetin alpha subunit [ADK22821]
Deinagkistrodon acutus Agglucetin subunit alpha [Q8JIV9]
Crotalus horridus CHH-B [P81508]
Deinagkistrodon acutus Agkicetin-C subunit alpha [Q9DEA2]
Opheodrys aestivus (SAL)
Anolis carolinensis c-type lectin BiL-like [XP 003223923]
Anolis carolinensis c-type lectin BFL-2-like [XP 003223920]
Homo sapiens C-type lectin [AAG00514]
Meleagris gallopavo c-type lectindomain family 2 member D-like [XP 003214104]
Gallus gallus C-type lectin [NP 001026644]
Rattus norvegicus C-type lectin domain family 4 member K [XP 002726471]
Homo sapiens C-type lectin domain family 4 member K [NP 056532]
Mus musculus C type lectin [CAC82936]
68
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73
32
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100
45
100
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41
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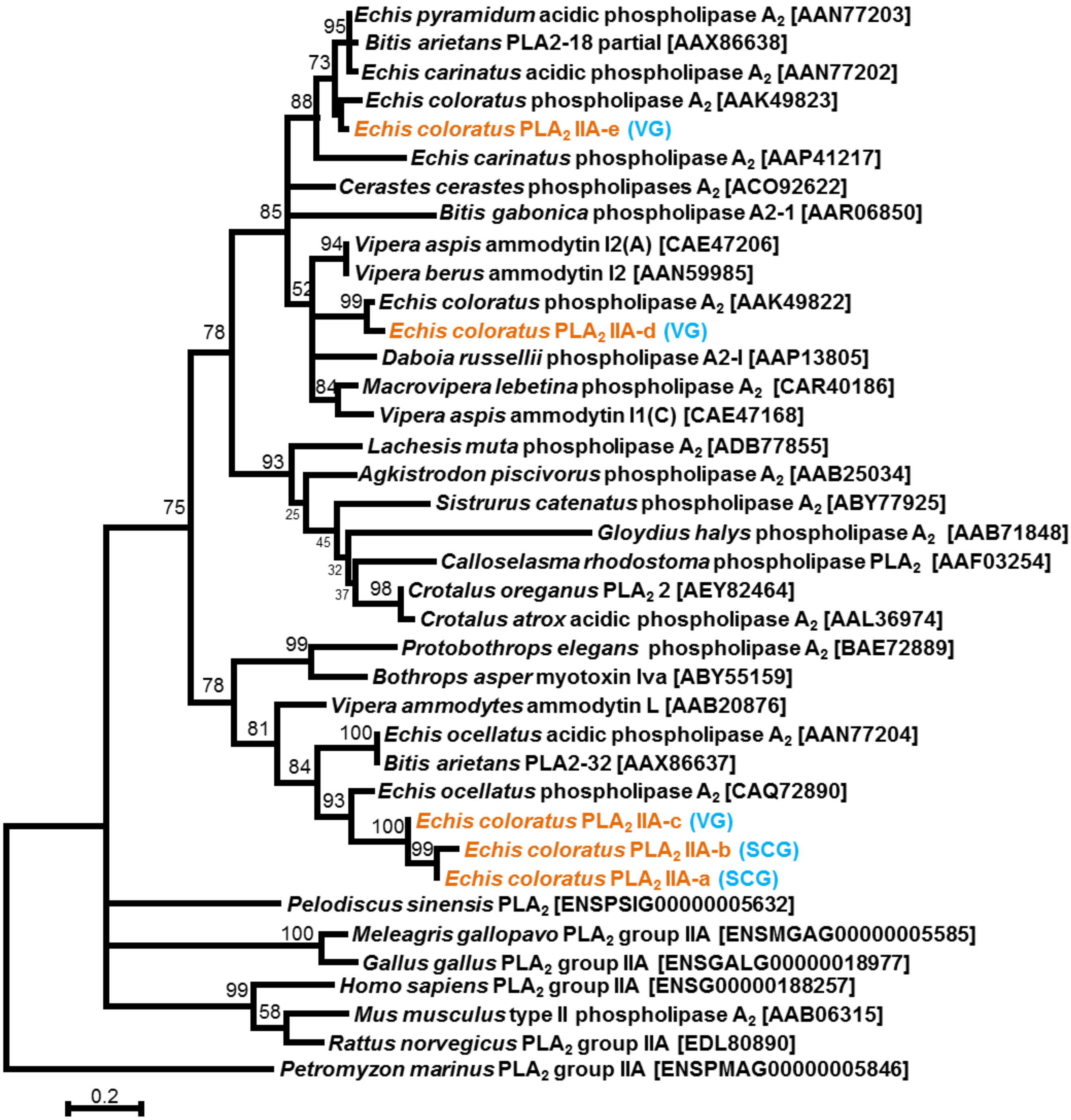
100
91
37
100
92
100
31
0.2

Supplementary figure S17

Maximum likelihood tree of *c-type lectin* (*ctl*) sequences. The putative viper venom-specific *ctl* clade is shaded green. Genbank accession numbers or Ensembl gene IDs are given in square brackets. Sequences from this study are in orange text and the location of transcripts is provided in bracketed blue text (VG, venom gland; SAL, salivary gland; SK, skin; SCG, scent gland). Numbers above branches correspond to Bootstrap values for 500 replicates


Echis pyramidum acidic phospholipase A_2 [AAN77203]
Bitis arietans PLA2-18 partial [AAX86638]
Echis carinatus acidic phospholipase A_2 [AAN77202]
Echis coloratus phospholipase A_2 [AAK49823]
Echis coloratus PLA$_2$ IIA-e (VG)
Echis carinatus phospholipase A_2 [AAP41217]
Cerastes cerastes phospholipases A_2 [ACO92622]
Bitis gabonica phospholipase A2-1 [AAR06850]
Vipera aspis ammodytin I2(A) [CAE47206]
Vipera berus ammodytin I2 [AAN59985]
Echis coloratus phospholipase A_2 [AAK49822]
Echis coloratus PLA$_2$ IIA-d (VG)
Daboia russellii phospholipase A2-I [AAP13805]
Macrovipera lebetina phospholipase A_2 [CAR40186]
Vipera aspis ammodytin I1(C) [CAE47168]
Lachesis muta phospholipase A_2 [ADB77855]
Agkistrodon piscivorus phospholipase A_2 [AAB25034]
Sistrurus catenatus phospholipase A_2 [ABY77925]
Gloydius halys phospholipase A_2 [AAB71848]
Calloselasma rhodostoma phospholipase PLA$_2$ [AAF03254]
Crotalus oreganus PLA$_2$ 2 [AEY82464]
Crotalus atrox acidic phospholipase A_2 [AAL36974]
Protobothrops elegans phospholipase A_2 [BAE72889]
Bothrops asper myotoxin Iva [ABY55159]
Vipera ammodytes ammodytin L [AAB20876]
Echis ocellatus acidic phospholipase A_2 [AAN77204]
Bitis arietans PLA2-32 [AAX86637]
Echis ocellatus phospholipase A_2 [CAQ72890]
Echis coloratus PLA$_2$ IIA-c (VG)
Echis coloratus PLA$_2$ IIA-b (SCG)
Echis coloratus PLA$_2$ IIA-a (SCG)
Pelodiscus sinensis PLA$_2$ [ENSPSIG00000005632]
Meleagris gallopavo PLA$_2$ group IIA [ENSMGAG00000005585]
Gallus gallus PLA$_2$ group IIA [ENSGALG00000018977]
Homo sapiens PLA$_2$ group IIA [ENSG00000188257]
Mus musculus type II phospholipase A_2 [AAB06315]
Rattus norvegicus PLA$_2$ group IIA [EDL80890]
Petromyzon marinus PLA$_2$ group IIA [ENSPMAG00000005846]
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81
100
84
93
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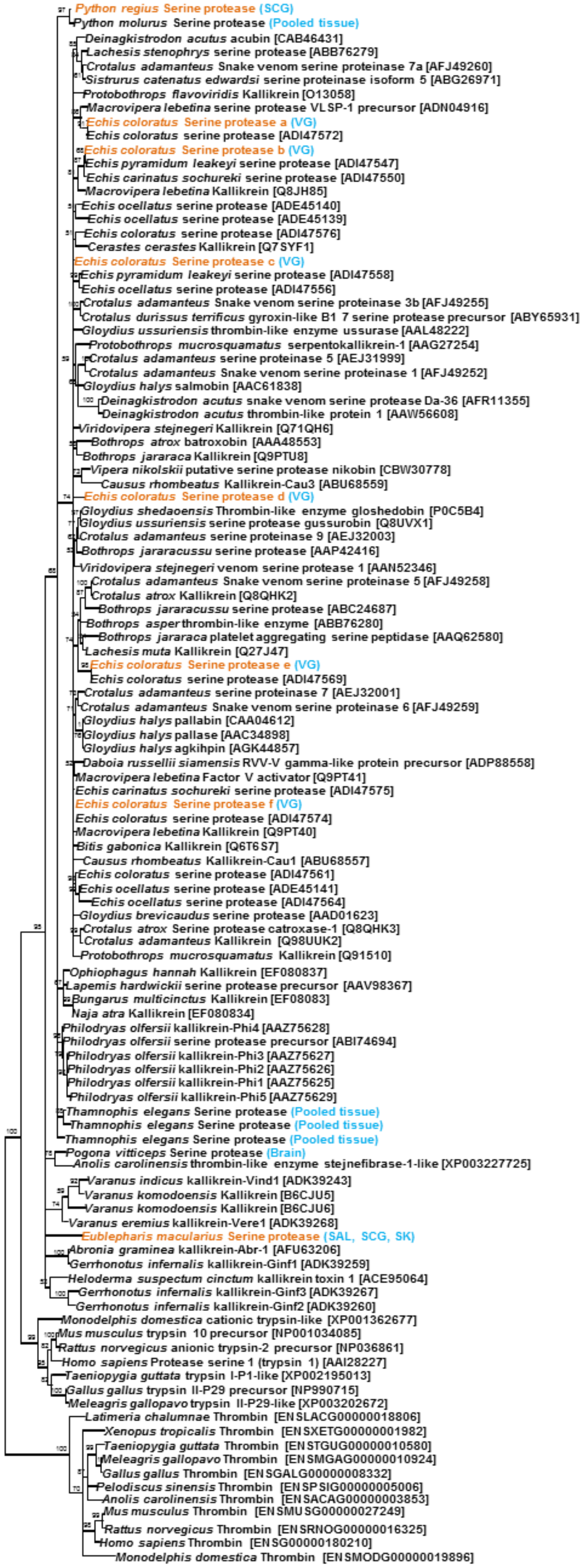
99
100
99
58
0.2

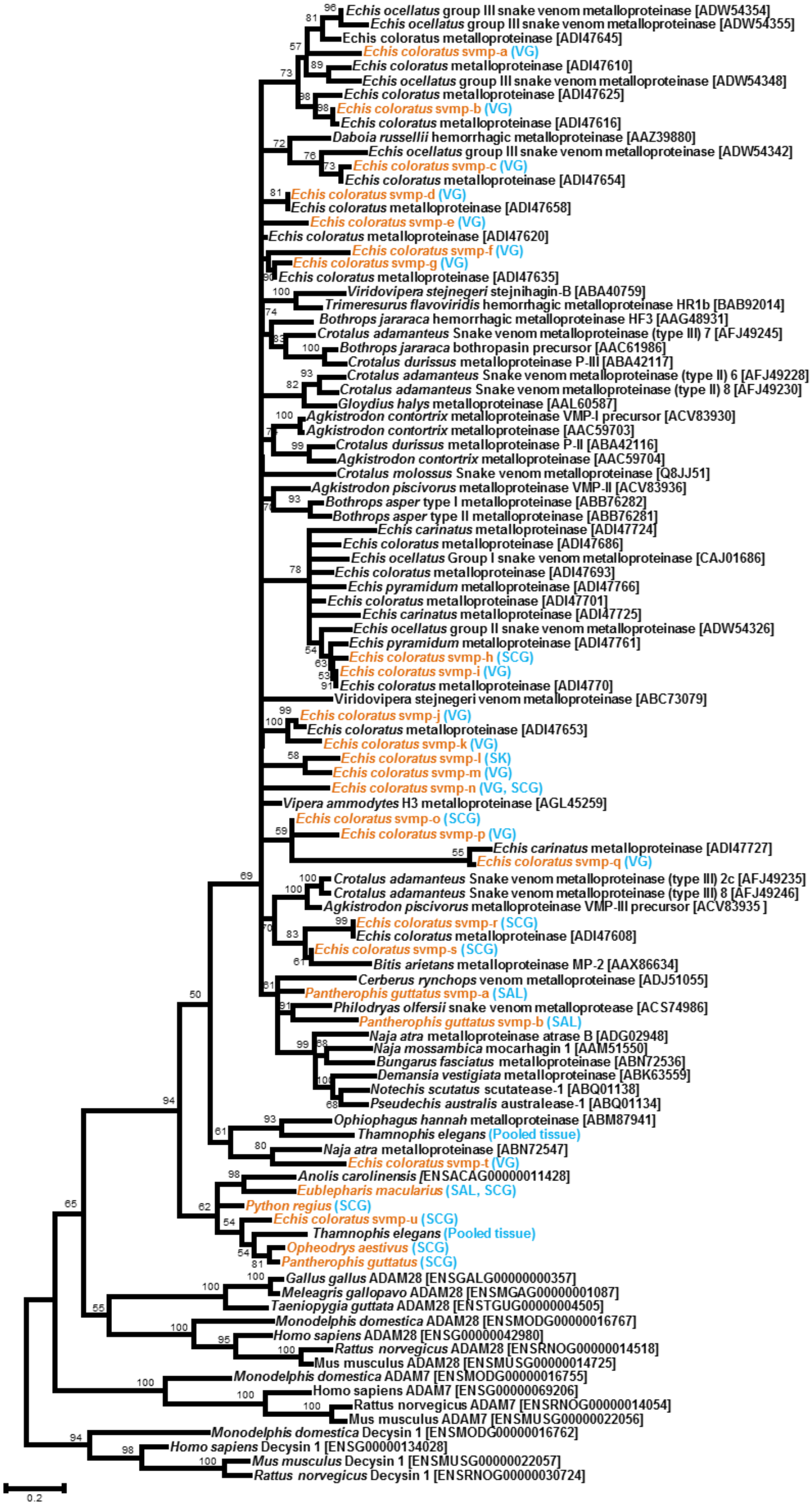
Supplementary figure S18

Maximum likelihood tree of *Group IIA Phospholipase* A_2 (*PLA*$_2$ *Group IIA*) sequences. Genbank accession numbers or Ensembl gene IDs are given in square brackets. Sequences from this study are in orange text and the location of transcripts is provided in bracketed blue text (VG, venom gland; SAL, salivary gland; SK, skin; SCG, scent gland). Numbers above branches correspond to Bootstrap values for 500 replicates. The *Echis coloratus* sequences for *PLA*$_2$ *IIA-a* and *IIA-b* are likely to be alleles or due to individual variation between samples used in this study, and probably represent the same gene.


Python regius Serine protease (SCG)
Python molurus Serine protease (Pooled tissue)
Deinagkistrodon acutus acubin [CAB46431]
Lachesis stenophrys serine protease [ABB76279]
Crotalus adamanteus Snake venom serine proteinase 7a [AFJ49260]
Sistrurus catenatus edwardsi serine proteinase isoform 5 [ABG26971]
Protobothrops flavoviridis Kallikrein [O13058]
Macrovipera lebetina serine protease VLSP-1 precursor [ADN04916]
Echis coloratus Serine protease a (VG)
Echis coloratus serine protease [ADI47572]
Echis coloratus Serine protease b (VG)
Echis pyramidum leakeyi serine protease [ADI47547]
Echis carinatus sochureki serine protease [ADI47550]
Macrovipera lebetina Kallikrein [Q8JH85]
Echis ocellatus serine protease [ADE45140]
Echis ocellatus serine protease [ADE45139]
Echis coloratus serine protease [ADI47576]
Cerastes cerastes Kallikrein [Q7SYF1]
Echis coloratus Serine protease c (VG)
Echis pyramidum leakeyi serine protease [ADI47558]
Echis ocellatus serine protease [ADI47556]
Crotalus adamanteus Snake venom serine proteinase 3b [AFJ49255]
Crotalus durissus terrificus gyroxin-like B1 7 serine protease precursor [ABY65931]
Gloydius ussuriensis thrombin-like enzyme ussurase [AAL48222]
Protobothrops mucrosquamatus serpentokallikrein-1 [AAG27254]
Crotalus adamanteus serine proteinase 5 [AEJ31999]
Crotalus adamanteus Snake venom serine proteinase 1 [AFJ49252]
Gloydius halys salmobin [AAC61838]
Deinagkistrodon acutus snake venom serine protease Da-36 [AFR11355]
Deinagkistrodon acutus thrombin-like protein 1 [AAW56608]
Viridovipera stejnegeri Kallikrein [Q71QH6]
Bothrops atrox batroxobin [AAA48553]
Bothrops jararaca Kallikrein [Q9PTU8]
Vipera nikolskii putative serine protease nikobin [CBW30778]
Causus rhombeatus Kallikrein-Cau3 [ABU68559]
Echis coloratus Serine protease d (VG)
Gloydius shedaoensis Thrombin-like enzyme gloshedobin [P0C5B4]
Gloydius ussuriensis serine protease gussurobin [Q8UVX1]
Crotalus adamanteus serine proteinase 9 [AEJ32003]
Bothrops jararacussu serine protease [AAP42416]
Viridovipera stejnegeri venom serine protease 1 [AAN52346]
Crotalus adamanteus Snake venom serine proteinase 5 [AFJ49258]
Crotalus atrox Kallikrein [Q8QHK2]
Bothrops jararacussu serine protease [ABC24687]
Bothrops asper thrombin-like enzyme [ABB76280]
Bothrops jararaca platelet aggregating serine peptidase [AAQ62580]
Lachesis muta Kallikrein [Q27J47]
Echis coloratus Serine protease e (VG)
Echis coloratus serine protease [ADI47569]
Crotalus adamanteus serine proteinase 7 [AEJ32001]
Crotalus adamanteus Snake venom serine proteinase 6 [AFJ49259]
Gloydius halys pallabin [CAA04612]
Gloydius halys pallase [AAC34898]
Gloydius halys agkihpin [AGK44857]
Daboia russellii siamensis RVV-V gamma-like protein precursor [ADP88558]
Macrovipera lebetina Factor V activator [Q9PT41]
Echis carinatus sochureki serine protease [ADI47575]
Echis coloratus Serine protease f (VG)
Echis coloratus serine protease [ADI47574]
Macrovipera lebetina Kallikrein [Q9PT40]
Bitis gabonica Kallikrein [Q6T6S7]
Causus rhombeatus Kallikrein-Cau1 [ABU68557]
Echis coloratus serine protease [ADI47561]
Echis ocellatus serine protease [ADE45141]
Echis ocellatus serine protease [ADI47564]
Gloydius brevicaudus serine protease [AAD01623]
Crotalus atrox Serine protease catroxase-1 [Q8QHK3]
Crotalus adamanteus Kallikrein [Q98UUK2]
Protobothrops mucrosquamatus Kallikrein [Q91510]
Ophiophagus hannah Kallikrein [EF080837]
Lapemis hardwickii serine protease precursor [AAV98367]
Bungarus multicinctus Kallikrein [EF08083]
Naja atra Kallikrein [EF080834]
Philodryas olfersii kallikrein-Phi4 [AAZ75628]
Philodryas olfersii serine protease precursor [ABI74694]
Philodryas olfersii kallikrein-Phi3 [AAZ75627]
Philodryas olfersii kallikrein-Phi2 [AAZ75626]
Philodryas olfersii kallikrein-Phi1 [AAZ75625]
Philodryas olfersii kallikrein-Phi5 [AAZ75629]
Thamnophis elegans Serine protease (Pooled tissue)
Thamnophis elegans Serine protease (Pooled tissue)
Thamnophis elegans Serine protease (Pooled tissue)
Pogona vitticeps Serine protease (Brain)
Anolis carolinensis thrombin-like enzyme stejnefibrase-1-like [XP003227725]
Varanus indicus kallikrein-Vind1 [ADK39243]
Varanus komodoensis Kallikrein [B6CJU5]
Varanus komodoensis Kallikrein [B6CJU6]
Varanus eremius kallikrein-Vere1 [ADK39268]
Eublepharis macularius Serine protease (SAL, SCG, SK)
Abronia graminea kallikrein-Abr-1 [AFU63206]
Gerrhonotus infernalis kallikrein-Ginf1 [ADK39259]
Heloderma suspectum cinctum kallikrein toxin 1 [ACE95064]
Gerrhonotus infernalis kallikrein-Ginf3 [ADK39267]
Gerrhonotus infernalis kallikrein-Ginf2 [ADK39260]
Monodelphis domestica cationic trypsin-like [XP001362677]
Mus musculus trypsin 10 precursor [NP001034085]
Rattus norvegicus anionic trypsin-2 precursor [NP036861]
Homo sapiens Protease serine 1 (trypsin 1) [AAI28227]
Taeniopygia guttata trypsin I-P1-like [XP002195013]
Gallus gallus trypsin II-P29 precursor [NP990715]
Meleagris gallopavo trypsin II-P29-like [XP003202672]
Latimeria chalumnae Thrombin [ENSLACG00000018806]
Xenopus tropicalis Thrombin [ENSXETG00000001982]
Taeniopygia guttata Thrombin [ENSTGUG00000010580]
Meleagris gallopavo Thrombin [ENSMGAG00000010924]
Gallus gallus Thrombin [ENSGALG00000008332]
Pelodiscus sinensis Thrombin [ENSPSIG00000005006]
Anolis carolinensis Thrombin [ENSACAG00000003853]
Mus musculus Thrombin [ENSMUSG00000027249]
Rattus norvegicus Thrombin [ENSRNOG00000016325]
Homo sapiens Thrombin [ENSG00000180210]
Monodelphis domestica Thrombin [ENSMODG00000019896]

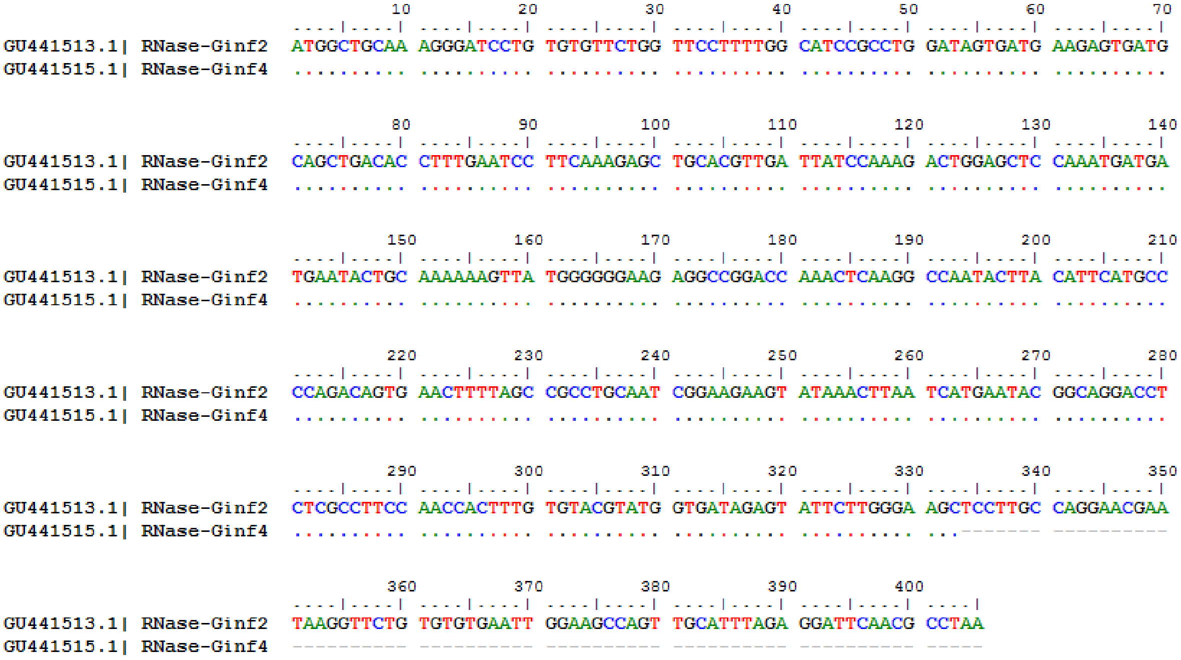
Supplementary figure S19

Maximum likelihood tree of *serine protease* (*sp*) genes. Genbank accession numbers or Ensembl gene IDs are given in square brackets. Sequences from this study are in orange text and the location of transcripts is provided in bracketed blue text (VG, venom gland; SAL, salivary gland; SK, skin; SCG, scent gland). Numbers above branches correspond to Bootstrap values for 500 replicates.


96
Echis ocellatus group III snake venom metalloproteinase [ADW54354]
81
Echis ocellatus group III snake venom metalloproteinase [ADW54355]
Echis coloratus metalloproteinase [ADI47645]
57
Echis coloratus svmp-a (VG)
89
73
Echis coloratus metalloproteinase [ADI47610]
Echis ocellatus group III snake venom metalloproteinase [ADW54348]
98
Echis coloratus metalloproteinase [ADI47625]
98
Echis coloratus svmp-b (VG)
Echis coloratus metalloproteinase [ADI47616]
72
Daboia russellii hemorrhagic metalloproteinase [AAZ39880]
76
Echis ocellatus group III snake venom metalloproteinase [ADW54342]
73
Echis coloratus svmp-c (VG)
Echis coloratus metalloproteinase [ADI47654]
81
Echis coloratus svmp-d (VG)
Echis coloratus metalloproteinase [ADI47658]
Echis coloratus svmp-e (VG)
Echis coloratus metalloproteinase [ADI47620]
Echis coloratus svmp-f (VG)
Echis coloratus svmp-g (VG)
90
Echis coloratus metalloproteinase [ADI47635]
100
Viridovipera stejnegeri stejnihagin-B [ABA40759]
Trimeresurus flavoviridis hemorrhagic metalloproteinase HR1b [BAB92014]
74
Bothrops jararaca hemorrhagic metalloproteinase HF3 [AAG48931]
83
Crotalus adamanteus Snake venom metalloproteinase (type III) 7 [AFJ49245]
100
Bothrops jararaca bothropasin precursor [AAC61986]
Crotalus durissus metalloproteinase P-III [ABA42117]
93
Crotalus adamanteus Snake venom metalloproteinase (type II) 6 [AFJ49228]
82
Crotalus adamanteus Snake venom metalloproteinase (type II) 8 [AFJ49230]
Gloydius halys metalloproteinase [AAL60587]
100
Agkistrodon contortrix metalloproteinase VMP-I precursor [ACV83930]
74
Agkistrodon contortrix metalloproteinase [AAC59703]
99
Crotalus durissus metalloproteinase P-II [ABA42116]
Agkistrodon contortrix metalloproteinase [AAC59704]
Crotalus molossus Snake venom metalloproteinase [Q8JJ51]
Agkistrodon piscivorus metalloproteinase VMP-II [ACV83936]
93
Bothrops asper type I metalloproteinase [ABB76282]
76
Bothrops asper type II metalloproteinase [ABB76281]
Echis carinatus metalloproteinase [ADI47724]
Echis coloratus metalloproteinase [ADI47686]
Echis ocellatus Group I snake venom metalloproteinase [CAJ01686]
78
Echis coloratus metalloproteinase [ADI47693]
Echis pyramidum metalloproteinase [ADI47766]
Echis coloratus metalloproteinase [ADI47701]
Echis carinatus metalloproteinase [ADI47725]
Echis ocellatus group II snake venom metalloproteinase [ADW54326]
54
Echis pyramidum metalloproteinase [ADI47761]
63
Echis coloratus svmp-h (SCG)
53
Echis coloratus svmp-i (VG)
91
Echis coloratus metalloproteinase [ADI4770]
Viridovipera stejnegeri venom metalloproteinase [ABC73079]
99
Echis coloratus svmp-j (VG)
100
Echis coloratus metalloproteinase [ADI47653]
Echis coloratus svmp-k (VG)
58
Echis coloratus svmp-l (SK)
Echis coloratus svmp-m (VG)
Echis coloratus svmp-n (VG, SCG)
Vipera ammodytes H3 metalloproteinase [AGL45259]
Echis coloratus svmp-o (SCG)
59
Echis coloratus svmp-p (VG)
55
Echis carinatus metalloproteinase [ADI47727]
Echis coloratus svmp-q (VG)
69
100
Crotalus adamanteus Snake venom metalloproteinase (type III) 2c [AFJ49235]
100
Crotalus adamanteus Snake venom metalloproteinase (type III) 8 [AFJ49246]
Agkistrodon piscivorus metalloproteinase VMP-III precursor [ACV83935]
99
Echis coloratus svmp-r (SCG)
70
83
Echis coloratus metalloproteinase [ADI47608]
Echis coloratus svmp-s (SCG)
61
Bitis arietans metalloproteinase MP-2 [AAX86634]
Cerberus rynchops venom metalloproteinase [ADJ51055]
81
Pantherophis guttatus svmp-a (SAL)
91
Philodryas olfersii snake venom metalloprotease [ACS74986]
50
Pantherophis guttatus svmp-b (SAL)
Naja atra metalloproteinase atrase B [ADG02948]
99
88
Naja mossambica mocarhagin 1 [AAM51550]
Bungarus fasciatus metalloproteinase [ABN72536]
Demansia vestigiata metalloproteinase [ABK63559]
100
Notechis scutatus scutatease-1 [ABQ01138]
68
Pseudechis australis australease-1 [ABQ01134]
94
93
Ophiophagus hannah metalloproteinase [ABM87941]
61
Thamnophis elegans (Pooled tissue)
80
Naja atra metalloproteinase [ABN72547]
Echis coloratus svmp-t (VG)
98
Anolis carolinensis [ENSACAG00000011428]
Eublepharis macularius (SAL, SCG)
65
62
Python regius (SCG)
54
Echis coloratus svmp-u (SCG)
Thamnophis elegans (Pooled tissue)
54
Opheodrys aestivus (SCG)
81
Pantherophis guttatus (SCG)
100
Gallus gallus ADAM28 [ENSGALG00000000357]
100
Meleagris gallopavo ADAM28 [ENSMGAG00000001087]
55
Taeniopygia guttata ADAM28 [ENSTGUG00000004505]
Monodelphis domestica ADAM28 [ENSMODG00000016767]
100
95
Homo sapiens ADAM28 [ENSG00000042980]
100
Rattus norvegicus ADAM28 [ENSRNOG00000014518]
Mus musculus ADAM28 [ENSMUSG00000014725]
100
Monodelphis domestica ADAM7 [ENSMODG00000016755]
100
Homo sapiens ADAM7 [ENSG00000069206]
100
Rattus norvegicus ADAM7 [ENSRNOG00000014054]
Mus musculus ADAM7 [ENSMUSG00000022056]
94
Monodelphis domestica Decysin 1 [ENSMODG00000016762]
98
Homo sapiens Decysin 1 [ENSG00000134028]
100
Mus musculus Decysin 1 [ENSMUSG00000022057]
Rattus norvegicus Decysin 1 [ENSRNOG00000030724]
0.2

Supplementary figure S20

Maximum likelihood tree of *snake venom metalloproteinase* (*svmp*) genes. Genbank accession numbers or Ensembl gene IDs are given in square brackets. Sequences from this study are in orange text and the location of transcripts is provided in bracketed blue text (VG, venom gland; SAL, salivary gland; SK, skin; SCG, scent gland). Numbers above branches correspond to Bootstrap values for 500 replicates.



```
                                   10         20         30         40         50         60         70
                         ....|....| ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
GU441513.1| RNase-Ginf2  ATGGCTGCAA AGGGATCCTG TGTGTTCTGG TTCCTTTTGG CATCCGCCTG GATAGTGATG AAGAGTGATG
GU441515.1| RNase-Ginf4  .......... .......... .......... .......... .......... .......... ..........

                                   80         90        100        110        120        130        140
                         ....|....| ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
GU441513.1| RNase-Ginf2  CAGCTGACAC CTTTGAATCC TTCAAAGAGC TGCACGTTGA TTATCCAAAG ACTGGAGCTC CAAATGATGA
GU441515.1| RNase-Ginf4  .......... .......... .......... .......... .......... .......... ..........

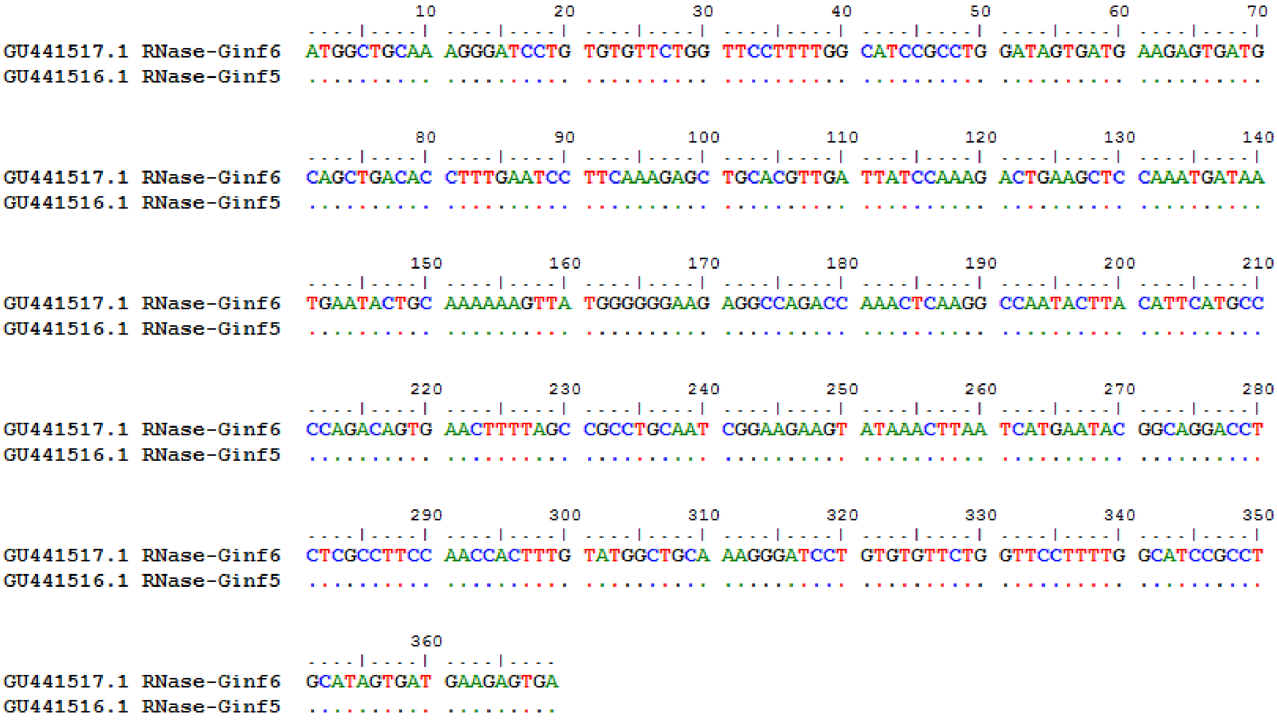
                                  150        160        170        180        190        200        210
                         ....|....| ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
GU441513.1| RNase-Ginf2  TGAATACTGC AAAAAAGTTA TGGGGGGAAG AGGCCGGACC AAACTCAAGG CCAATACTTA CATTCATGCC
GU441515.1| RNase-Ginf4  .......... .......... .......... .......... .......... .......... ..........

                                  220        230        240        250        260        270        280
                         ....|....| ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
GU441513.1| RNase-Ginf2  CCAGACAGTG AACTTTTAGC CGCCTGCAAT CGGAAGAAGT ATAAACTTAA TCATGAATAC GGCAGGACCT
GU441515.1| RNase-Ginf4  .......... .......... .......... .......... .......... .......... ..........

                                  290        300        310        320        330        340        350
                         ....|....| ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
GU441513.1| RNase-Ginf2  CTCGCCTTCC AACCACTTTG TGTACGTATG GTGATAGAGT ATTCTTGGGA AGCTCCTTGC CAGGAACGAA
GU441515.1| RNase-Ginf4  .......... .......... .......... .......... .......... ...------- ----------

                                  360        370        380        390        400
                         ....|....| ....|....| ....|....| ....|....| ....|....| ....|
GU441513.1| RNase-Ginf2  TAAGGTTCTG TGTGTGAATT GGAAGCCAGT TGCATTTAGA GGATTCAACG CCTAA
GU441515.1| RNase-Ginf4  ---------- ---------- ---------- ---------- ---------- -----
```

Supplementary figure S21. Alignments of *Gerrhonotus infernalis* ribonuclease sequences [3] GU441513 (“Ginf2”) and GU441515 (“Ginf4”) showing 100% similarity at the nucleotide level. Sequence lengths reflect those on Genbank and have not been edited.



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                                10         20         30         40         50         60         70
                        ....|....| ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
GU441517.1 RNase-Ginf6  ATGGCTGCAA AGGGATCCTG TGTGTTCTGG TTCCTTTTGG CATCCGCCTG GATAGTGATG AAGAGTGATG
GU441516.1 RNase-Ginf5  .......... .......... .......... .......... .......... .......... ..........

                                80         90        100        110        120        130        140
                        ....|....| ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
GU441517.1 RNase-Ginf6  CAGCTGACAC CTTTGAATCC TTCAAAGAGC TGCACGTTGA TTATCCAAAG ACTGAAGCTC CAAATGATAA
GU441516.1 RNase-Ginf5  .......... .......... .......... .......... .......... .......... ..........

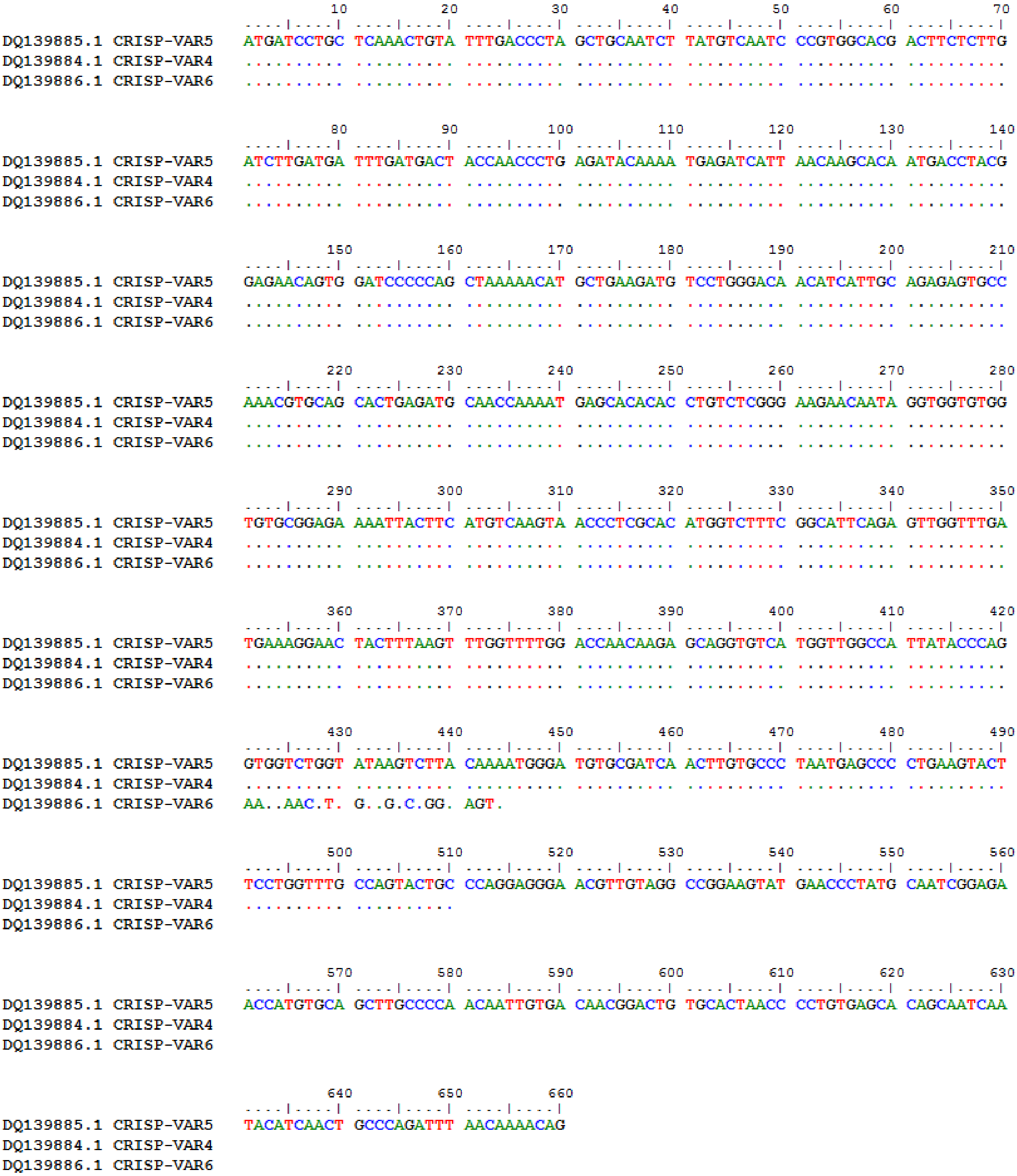
                               150        160        170        180        190        200        210
                        ....|....| ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
GU441517.1 RNase-Ginf6  TGAATACTGC AAAAAAGTTA TGGGGGGAAG AGGCCAGACC AAACTCAAGG CCAATACTTA CATTCATGCC
GU441516.1 RNase-Ginf5  .......... .......... .......... .......... .......... .......... ..........

                               220        230        240        250        260        270        280
                        ....|....| ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
GU441517.1 RNase-Ginf6  CCAGACAGTG AACTTTTAGC CGCCTGCAAT CGGAAGAAGT ATAAACTTAA TCATGAATAC GGCAGGACCT
GU441516.1 RNase-Ginf5  .......... .......... .......... .......... .......... .......... ..........

                               290        300        310        320        330        340        350
                        ....|....| ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
GU441517.1 RNase-Ginf6  CTCGCCTTCC AACCACTTTG TATGGCTGCA AAGGGATCCT GTGTGTTCTG GTTCCTTTTG GCATCCGCCT
GU441516.1 RNase-Ginf5  .......... .......... .......... .......... .......... .......... ..........

                               360
                        ....|....| ....|....
GU441517.1 RNase-Ginf6  GCATAGTGAT GAAGAGTGA
GU441516.1 RNase-Ginf5  .......... .........
```

Supplementary figure S22. Alignments of *Gerrhonotus infernalis* ribonuclease sequences [3] GU441516 (“Ginf5”) and GU441517 (“Ginf6”) showing 100% similarity at the nucleotide level. Sequence lengths reflect those on Genbank and have not been edited.



```
                                 10         20         30         40         50         60         70
                         ....|....| ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
DQ139885.1 CRISP-VAR5    ATGATCCTGC TCAAACTGTA TTTGACCCTA GCTGCAATCT TATGTCAATC CCGTGGCACG ACTTCTCTTG
DQ139884.1 CRISP-VAR4    .......... .......... .......... .......... .......... .......... ..........
DQ139886.1 CRISP-VAR6    .......... .......... .......... .......... .......... .......... ..........

                                 80         90        100        110        120        130        140
                         ....|....| ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
DQ139885.1 CRISP-VAR5    ATCTTGATGA TTTGATGACT ACCAACCCTG AGATACAAAA TGAGATCATT AACAAGCACA ATGACCTACG
DQ139884.1 CRISP-VAR4    .......... .......... .......... .......... .......... .......... ..........
DQ139886.1 CRISP-VAR6    .......... .......... .......... .......... .......... .......... ..........

                                150        160        170        180        190        200        210
                         ....|....| ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
DQ139885.1 CRISP-VAR5    GAGAACAGTG GATCCCCCAG CTAAAAACAT GCTGAAGATG TCCTGGGACA ACATCATTGC AGAGAGTGCC
DQ139884.1 CRISP-VAR4    .......... .......... .......... .......... .......... .......... ..........
DQ139886.1 CRISP-VAR6    .......... .......... .......... .......... .......... .......... ..........

                                220        230        240        250        260        270        280
                         ....|....| ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
DQ139885.1 CRISP-VAR5    AAACGTGCAG CACTGAGATG CAACCAAAAT GAGCACACAC CTGTCTCGGG AAGAACAATA GGTGGTGTGG
DQ139884.1 CRISP-VAR4    .......... .......... .......... .......... .......... .......... ..........
DQ139886.1 CRISP-VAR6    .......... .......... .......... .......... .......... .......... ..........

                                290        300        310        320        330        340        350
                         ....|....| ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
DQ139885.1 CRISP-VAR5    TGTGCGGAGA AAATTACTTC ATGTCAAGTA ACCCTCGCAC ATGGTCTTTC GGCATTCAGA GTTGGTTTGA
DQ139884.1 CRISP-VAR4    .......... .......... .......... .......... .......... .......... ..........
DQ139886.1 CRISP-VAR6    .......... .......... .......... .......... .......... .......... ..........

                                360        370        380        390        400        410        420
                         ....|....| ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
DQ139885.1 CRISP-VAR5    TGAAAGGAAC TACTTTAAGT TTGGTTTTGG ACCAACAAGA GCAGGTGTCA TGGTTGGCCA TTATACCCAG
DQ139884.1 CRISP-VAR4    .......... .......... .......... .......... .......... .......... ..........
DQ139886.1 CRISP-VAR6    .......... .......... .......... .......... .......... .......... ..........

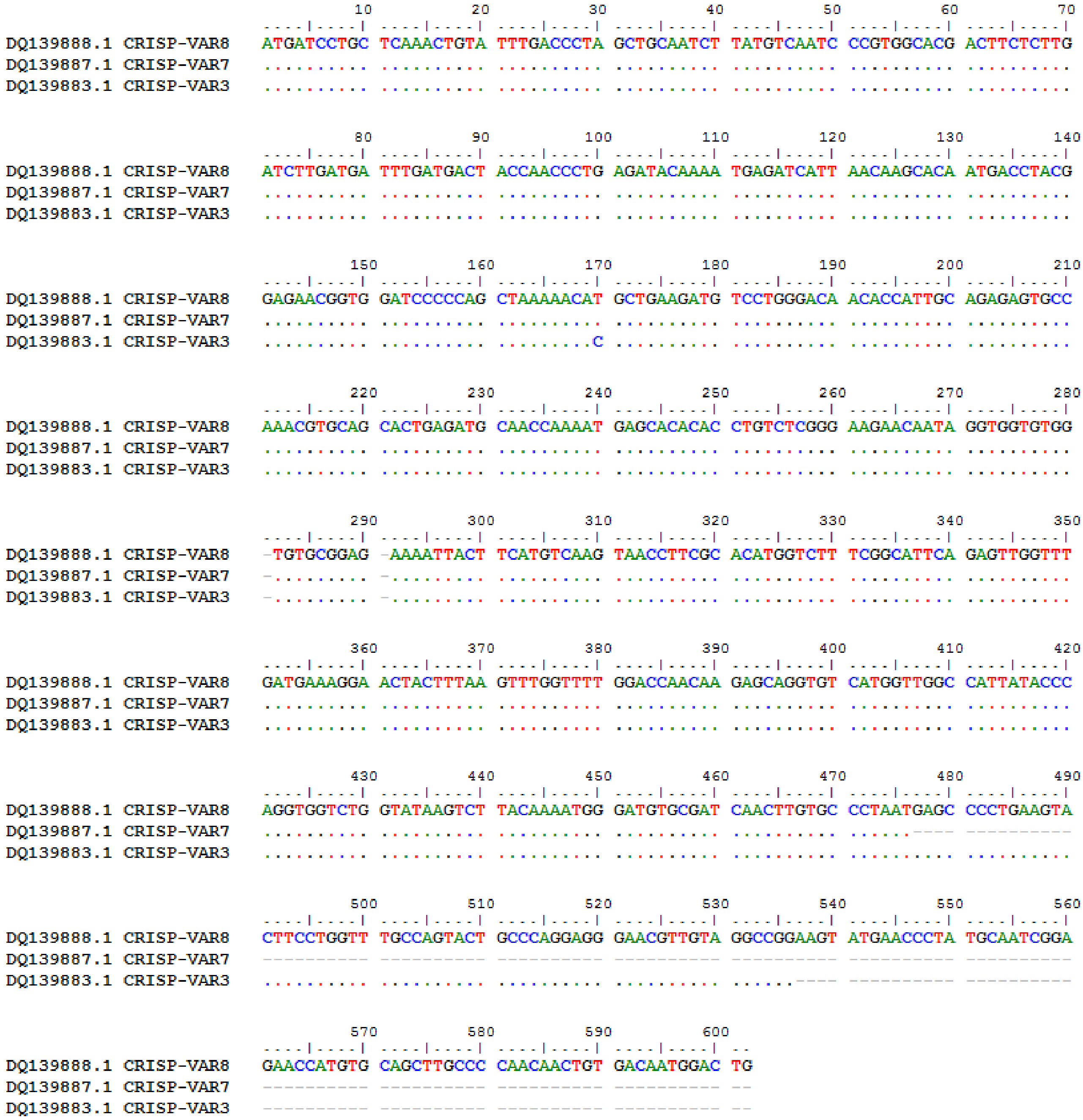
                                430        440        450        460        470        480        490
                         ....|....| ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
DQ139885.1 CRISP-VAR5    GTGGTCTGGT ATAAGTCTTA CAAAATGGGA TGTGCGATCA ACTTGTGCCC TAATGAGCCC CTGAAGTACT
DQ139884.1 CRISP-VAR4    .......... .......... .......... .......... .......... .......... ..........
DQ139886.1 CRISP-VAR6    AA..AAC.T. G..G.C.GG. AGT.

                                500        510        520        530        540        550        560
                         ....|....| ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
DQ139885.1 CRISP-VAR5    TCCTGGTTTG CCAGTACTGC CCAGGAGGGA ACGTTGTAGG CCGGAAGTAT GAACCCTATG CAATCGGAGA
DQ139884.1 CRISP-VAR4    .......... ..........
DQ139886.1 CRISP-VAR6

                                570        580        590        600        610        620        630
                         ....|....| ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
DQ139885.1 CRISP-VAR5    ACCATGTGCA GCTTGCCCCA ACAATTGTGA CAACGGACTG TGCACTAACC CCTGTGAGCA CAGCAATCAA
DQ139884.1 CRISP-VAR4
DQ139886.1 CRISP-VAR6

                                640        650        660
                         ....|....| ....|....| ....|....|
DQ139885.1 CRISP-VAR5    TACATCAACT GCCCAGATTT AACAAAACAG
DQ139884.1 CRISP-VAR4
DQ139886.1 CRISP-VAR6
```

Supplementary figure S23. Nucleotide alignments of *Varanus acanthurus* CRISP sequences [4] DQ139885 ("CRISP-VAR5"), DQ139884 ("CRISP-VAR4") and DQ139886 ("CRISP-VAR6") showing almost total similarity at the nucleotide level. Sequence lengths reflect those on Genbank and have not been edited.



```
                                 10         20         30         40         50         60         70
                         ....|....| ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
DQ139888.1 CRISP-VAR8    ATGATCCTGC TCAAACTGTA TTTGACCCTA GCTGCAATCT TATGTCAATC CCGTGGCACG ACTTCTCTTG
DQ139887.1 CRISP-VAR7    .......... .......... .......... .......... .......... .......... ..........
DQ139883.1 CRISP-VAR3    .......... .......... .......... .......... .......... .......... ..........

                                 80         90        100        110        120        130        140
                         ....|....| ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
DQ139888.1 CRISP-VAR8    ATCTTGATGA TTTGATGACT ACCAACCCTG AGATACAAAA TGAGATCATT AACAAGCACA ATGACCTACG
DQ139887.1 CRISP-VAR7    .......... .......... .......... .......... .......... .......... ..........
DQ139883.1 CRISP-VAR3    .......... .......... .......... .......... .......... .......... ..........

                                150        160        170        180        190        200        210
                         ....|....| ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
DQ139888.1 CRISP-VAR8    GAGAACGGTG GATCCCCCAG CTAAAAACAT GCTGAAGATG TCCTGGGACA ACACCATTGC AGAGAGTGCC
DQ139887.1 CRISP-VAR7    .......... .......... .......... .......... .......... .......... ..........
DQ139883.1 CRISP-VAR3    .......... .......... .........C .......... .......... .......... ..........

                                220        230        240        250        260        270        280
                         ....|....| ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
DQ139888.1 CRISP-VAR8    AAACGTGCAG CACTGAGATG CAACCAAAAT GAGCACACAC CTGTCTCGGG AAGAACAATA GGTGGTGTGG
DQ139887.1 CRISP-VAR7    .......... .......... .......... .......... .......... .......... ..........
DQ139883.1 CRISP-VAR3    .......... .......... .......... .......... .......... .......... ..........

                                290        300        310        320        330        340        350
                         ....|....| ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
DQ139888.1 CRISP-VAR8    -TGTGCGGAG -AAAATTACT TCATGTCAAG TAACCTTCGC ACATGGTCTT TCGGCATTCA GAGTTGGTTT
DQ139887.1 CRISP-VAR7    -......... -......... .......... .......... .......... .......... ..........
DQ139883.1 CRISP-VAR3    -......... -......... .......... .......... .......... .......... ..........

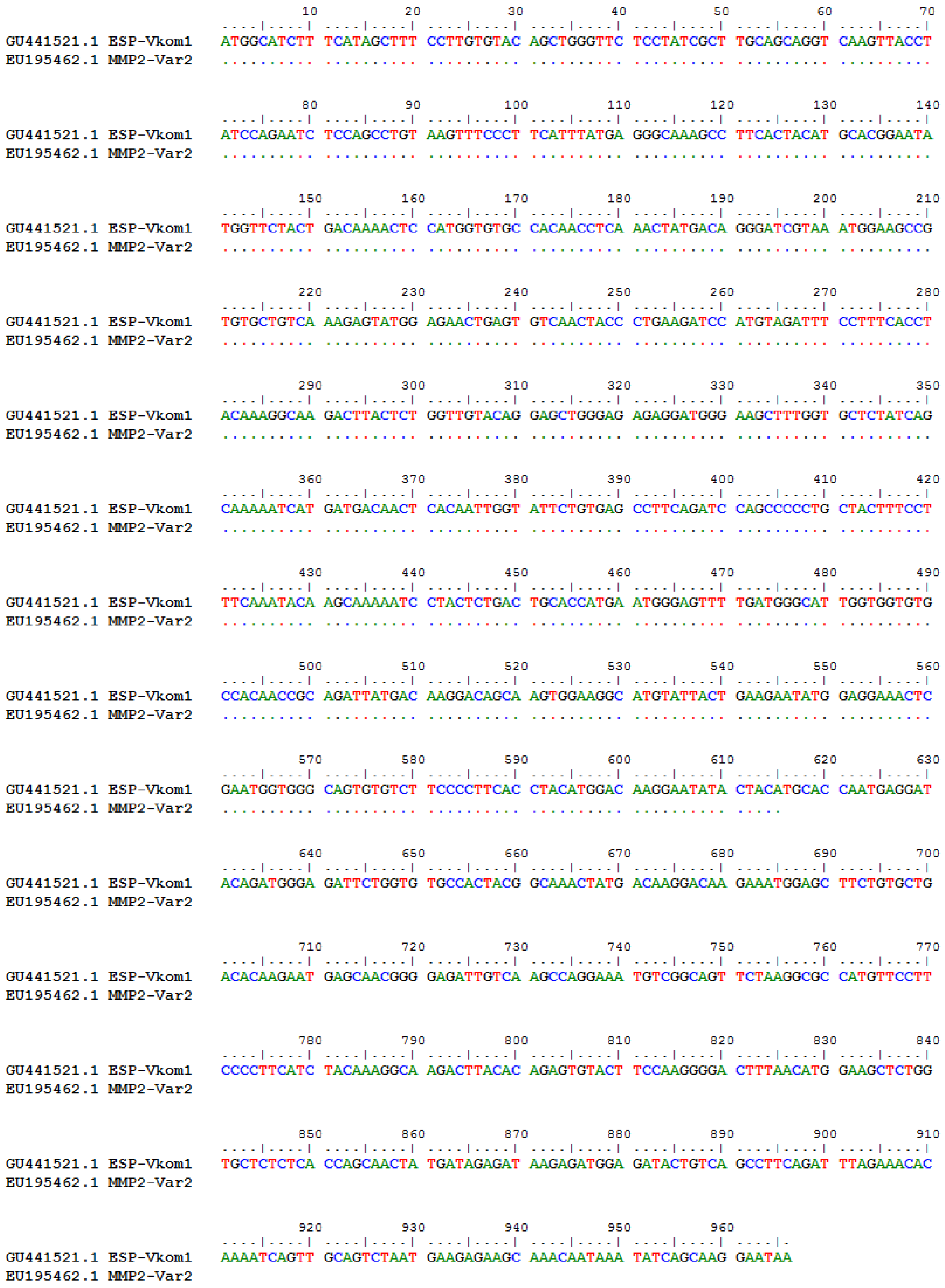
                                360        370        380        390        400        410        420
                         ....|....| ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
DQ139888.1 CRISP-VAR8    GATGAAAGGA ACTACTTTAA GTTTGGTTTT GGACCAACAA GAGCAGGTGT CATGGTTGGC CATTATACCC
DQ139887.1 CRISP-VAR7    .......... .......... .......... .......... .......... .......... ..........
DQ139883.1 CRISP-VAR3    .......... .......... .......... .......... .......... .......... ..........

                                430        440        450        460        470        480        490
                         ....|....| ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
DQ139888.1 CRISP-VAR8    AGGTGGTCTG GTATAAGTCT TACAAAATGG GATGTGCGAT CAACTTGTGC CCTAATGAGC CCCTGAAGTA
DQ139887.1 CRISP-VAR7    .......... .......... .......... .......... .......... ......---- ----------
DQ139883.1 CRISP-VAR3    .......... .......... .......... .......... .......... .......... ..........

                                500        510        520        530        540        550        560
                         ....|....| ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
DQ139888.1 CRISP-VAR8    CTTCCTGGTT TGCCAGTACT GCCCAGGAGG GAACGTTGTA GGCCGGAAGT ATGAACCCTA TGCAATCGGA
DQ139887.1 CRISP-VAR7    ---------- ---------- ---------- ---------- ---------- ---------- ----------
DQ139883.1 CRISP-VAR3    .......... .......... .......... .......... ......---- ---------- ----------

                                570        580        590        600
                         ....|....| ....|....| ....|....| ....|....| ..
DQ139888.1 CRISP-VAR8    GAACCATGTG CAGCTTGCCC CAACAACTGT GACAATGGAC TG
DQ139887.1 CRISP-VAR7    ---------- ---------- ---------- ---------- --
DQ139883.1 CRISP-VAR3    ---------- ---------- ---------- ---------- --
```

Supplementary figure S24. Nucleotide alignments of *Varanus acanthurus* CRISP sequences [4] DQ139888 ("CRISP-VAR8"), DQ139887 ("CRISP-VAR7") and DQ139883 ("CRISP-VAR3") showing almost total similarity at the nucleotide level. Sequence lengths reflect those on Genbank and have not been edited.



```
                               10         20         30         40         50         60         70
                       ....|....| ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
GU441521.1 ESP-Vkom1   ATGGCATCTT TCATAGCTTT CCTTGTGTAC AGCTGGGTTC TCCTATCGCT TGCAGCAGGT CAAGTTACCT
EU195462.1 MMP2-Var2   .......... .......... .......... .......... .......... .......... ..........

                               80         90        100        110        120        130        140
                       ....|....| ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
GU441521.1 ESP-Vkom1   ATCCAGAATC TCCAGCCTGT AAGTTTCCCT TCATTTATGA GGGCAAAGCC TTCACTACAT GCACGGAATA
EU195462.1 MMP2-Var2   .......... .......... .......... .......... .......... .......... ..........

                              150        160        170        180        190        200        210
                       ....|....| ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
GU441521.1 ESP-Vkom1   TGGTTCTACT GACAAAACTC CATGGTGTGC CACAACCTCA AACTATGACA GGGATCGTAA ATGGAAGCCG
EU195462.1 MMP2-Var2   .......... .......... .......... .......... .......... .......... ..........

                              220        230        240        250        260        270        280
                       ....|....| ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
GU441521.1 ESP-Vkom1   TGTGCTGTCA AAGAGTATGG AGAACTGAGT GTCAACTACC CTGAAGATCC ATGTAGATTT CCTTTCACCT
EU195462.1 MMP2-Var2   .......... .......... .......... .......... .......... .......... ..........

                              290        300        310        320        330        340        350
                       ....|....| ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
GU441521.1 ESP-Vkom1   ACAAAGGCAA GACTTACTCT GGTTGTACAG GAGCTGGGAG AGAGGATGGG AAGCTTTGGT GCTCTATCAG
EU195462.1 MMP2-Var2   .......... .......... .......... .......... .......... .......... ..........

                              360        370        380        390        400        410        420
                       ....|....| ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
GU441521.1 ESP-Vkom1   CAAAAATCAT GATGACAACT CACAATTGGT ATTCTGTGAG CCTTCAGATC CAGCCCCCTG CTACTTTCCT
EU195462.1 MMP2-Var2   .......... .......... .......... .......... .......... .......... ..........

                              430        440        450        460        470        480        490
                       ....|....| ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
GU441521.1 ESP-Vkom1   TTCAAATACA AGCAAAAATC CTACTCTGAC TGCACCATGA ATGGGAGTTT TGATGGGCAT TGGTGGTGTG
EU195462.1 MMP2-Var2   .......... .......... .......... .......... .......... .......... ..........

                              500        510        520        530        540        550        560
                       ....|....| ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
GU441521.1 ESP-Vkom1   CCACAACCGC AGATTATGAC AAGGACAGCA AGTGGAAGGC ATGTATTACT GAAGAATATG GAGGAAACTC
EU195462.1 MMP2-Var2   .......... .......... .......... .......... .......... .......... ..........

                              570        580        590        600        610        620        630
                       ....|....| ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
GU441521.1 ESP-Vkom1   GAATGGTGGG CAGTGTGTCT TCCCCTTCAC CTACATGGAC AAGGAATATA CTACATGCAC CAATGAGGAT
EU195462.1 MMP2-Var2   .......... .......... .......... .......... .......... .....

                              640        650        660        670        680        690        700
                       ....|....| ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
GU441521.1 ESP-Vkom1   ACAGATGGGA GATTCTGGTG TGCCACTACG GCAAACTATG ACAAGGACAA GAAATGGAGC TTCTGTGCTG
EU195462.1 MMP2-Var2

                              710        720        730        740        750        760        770
                       ....|....| ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
GU441521.1 ESP-Vkom1   ACACAAGAAT GAGCAACGGG GAGATTGTCA AGCCAGGAAA TGTCGGCAGT TCTAAGGCGC CATGTTCCTT
EU195462.1 MMP2-Var2

                              780        790        800        810        820        830        840
                       ....|....| ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
GU441521.1 ESP-Vkom1   CCCCTTCATC TACAAAGGCA AGACTTACAC AGAGTGTACT TCCAAGGGGA CTTTAACATG GAAGCTCTGG
EU195462.1 MMP2-Var2

                              850        860        870        880        890        900        910
                       ....|....| ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
GU441521.1 ESP-Vkom1   TGCTCTCTCA CCAGCAACTA TGATAGAGAT AAGAGATGGA GATACTGTCA GCCTTCAGAT TTAGAAACAC
EU195462.1 MMP2-Var2

                              920        930        940        950        960
                       ....|....| ....|....| ....|....| ....|....| ....|....| ....|.
GU441521.1 ESP-Vkom1   AAAATCAGTT GCAGTCTAAT GAAGAGAAGC AAACAATAAA TATCAGCAAG GAATAA
EU195462.1 MMP2-Var2
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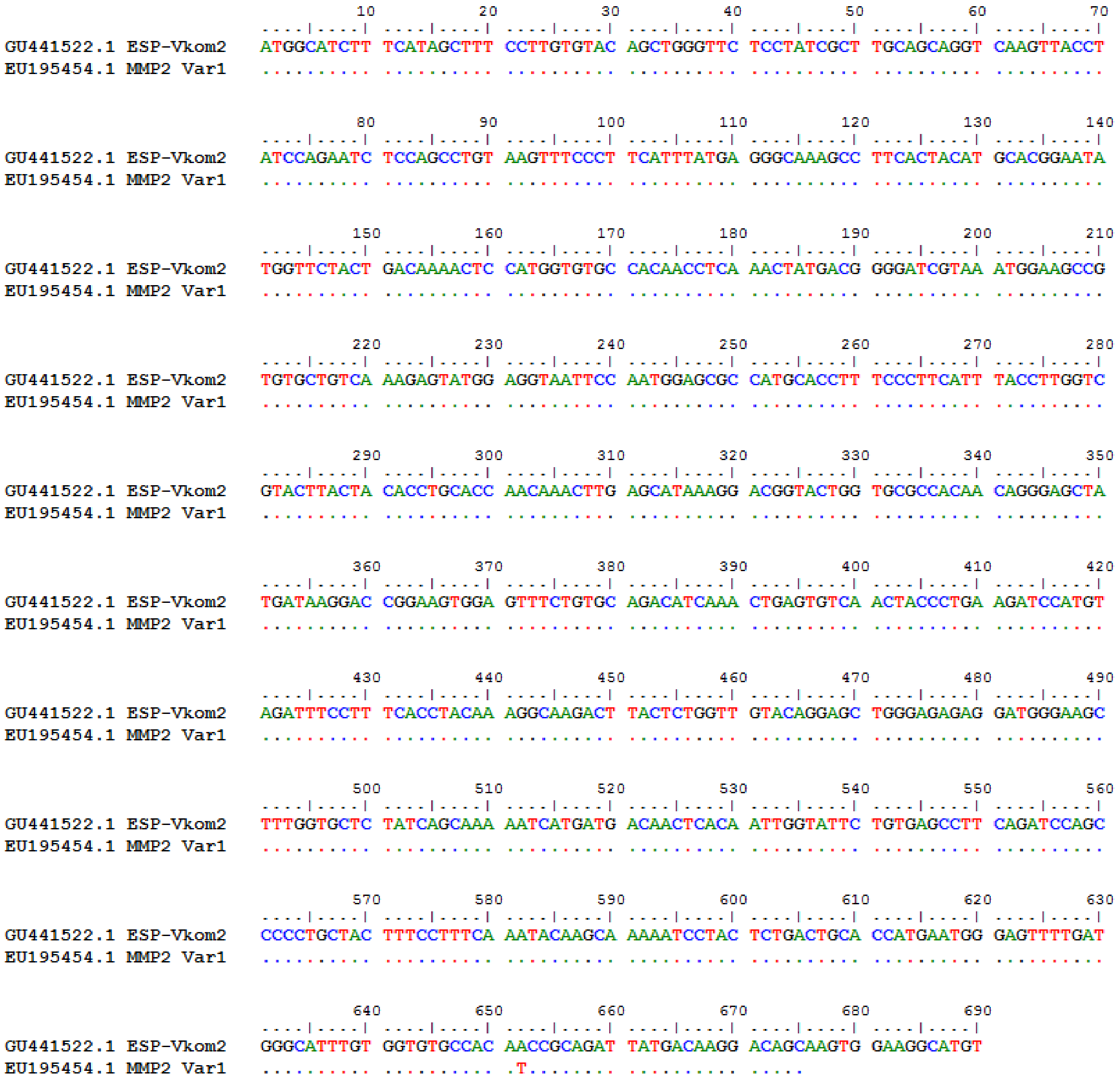
Supplementary figure S25. Alignments of *Varanus komodoensis* epididymal secretory protein (GU441521, “ESP-Vkom1”) and matrix metalloproteinase (EU195462, MMP2-Var2) sequences [3] showing 100% similarity at the nucleotide level. Sequence lengths reflect those on Genbank and have not been edited.



```
                               10         20         30         40         50         60         70
                       ....|....| ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
GU441522.1 ESP-Vkom2   ATGGCATCTT TCATAGCTTT CCTTGTGTAC AGCTGGGTTC TCCTATCGCT TGCAGCAGGT CAAGTTACCT
EU195454.1 MMP2 Var1   .......... .......... .......... .......... .......... .......... ..........

                               80         90        100        110        120        130        140
                       ....|....| ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
GU441522.1 ESP-Vkom2   ATCCAGAATC TCCAGCCTGT AAGTTTCCCT TCATTTATGA GGGCAAAGCC TTCACTACAT GCACGGAATA
EU195454.1 MMP2 Var1   .......... .......... .......... .......... .......... .......... ..........

                              150        160        170        180        190        200        210
                       ....|....| ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
GU441522.1 ESP-Vkom2   TGGTTCTACT GACAAAACTC CATGGTGTGC CACAACCTCA AACTATGACG GGGATCGTAA ATGGAAGCCG
EU195454.1 MMP2 Var1   .......... .......... .......... .......... .......... .......... ..........

                              220        230        240        250        260        270        280
                       ....|....| ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
GU441522.1 ESP-Vkom2   TGTGCTGTCA AAGAGTATGG AGGTAATTCC AATGGAGCGC CATGCACCTT TCCCTTCATT TACCTTGGTC
EU195454.1 MMP2 Var1   .......... .......... .......... .......... .......... .......... ..........

                              290        300        310        320        330        340        350
                       ....|....| ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
GU441522.1 ESP-Vkom2   GTACTTACTA CACCTGCACC AACAAACTTG AGCATAAAGG ACGGTACTGG TGCGCCACAA CAGGGAGCTA
EU195454.1 MMP2 Var1   .......... .......... .......... .......... .......... .......... ..........

                              360        370        380        390        400        410        420
                       ....|....| ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
GU441522.1 ESP-Vkom2   TGATAAGGAC CGGAAGTGGA GTTTCTGTGC AGACATCAAA CTGAGTGTCA ACTACCCTGA AGATCCATGT
EU195454.1 MMP2 Var1   .......... .......... .......... .......... .......... .......... ..........

                              430        440        450        460        470        480        490
                       ....|....| ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
GU441522.1 ESP-Vkom2   AGATTTCCTT TCACCTACAA AGGCAAGACT TACTCTGGTT GTACAGGAGC TGGGAGAGAG GATGGGAAGC
EU195454.1 MMP2 Var1   .......... .......... .......... .......... .......... .......... ..........

                              500        510        520        530        540        550        560
                       ....|....| ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
GU441522.1 ESP-Vkom2   TTTGGTGCTC TATCAGCAAA AATCATGATG ACAACTCACA ATTGGTATTC TGTGAGCCTT CAGATCCAGC
EU195454.1 MMP2 Var1   .......... .......... .......... .......... .......... .......... ..........

                              570        580        590        600        610        620        630
                       ....|....| ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
GU441522.1 ESP-Vkom2   CCCCTGCTAC TTTCCTTTCA AATACAAGCA AAAATCCTAC TCTGACTGCA CCATGAATGG GAGTTTTGAT
EU195454.1 MMP2 Var1   .......... .......... .......... .......... .......... .......... ..........

                              640        650        660        670        680        690
                       ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
GU441522.1 ESP-Vkom2   GGGCATTTGT GGTGTGCCAC AACCGCAGAT TATGACAAGG ACAGCAAGTG GAAGGCATGT
EU195454.1 MMP2 Var1   .......... .......... .T........ .......... .....
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Supplementary figure S26. Alignments of *Varanus komodoensis* epididymal secretory protein (GU441522, "ESP-Vkom2") and matrix metalloproteinase (EU195454, MMP2 Var1) nucleotide sequences [3] showing near total sequence identity (1bp difference over 675bp of aligned sequence). Sequence lengths reflect those on Genbank and have not been edited.

References for Supplementary material

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